

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: June 9, 2003, 08:36:50 ; Search time 474 Seconds
(without alignments)
1289.385 Million cell updates/sec

Title: US-09-550-163-1_COPY_230_250

Perfect score: 21

Sequence: 1 ctcatgtgatgattgaatg 21

Scoring table: IDENTITY NWC

Gapop 10.0 , Gapext 1.0

Searched: 2056440 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hvg.*

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4: gb_in.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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11: gb_sts.*

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13: gb_vl.*

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15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mus.*

20: em_mus.*

21: em_mus.*

22: em_ov.*

23: em_pat.*

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25: em_pl.*

26: em_ro.*

27: em_sts.*

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29: em_vl.*

30: em_htg_hum.*

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33: em_htg_mus.*

34: em_htg_pln.*

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37: em_htg_mam.*

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39: em_htg_hum.*

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	732	6	AX0406939	Sequence
2	21	100.0	732	6	AX0406947	Sequence
3	21	100.0	732	6	AX0406947	Sequence
4	21	100.0	732	6	AF071002	Homo sapi
5	21	100.0	809	9	AF302095	Homo sapi
6	21	100.0	24608	9	AF000320	Homo sapi
7	21	100.0	100000	9	AF000052	Homo sapi
8	21	100.0	100000	9	AF000167	Homo sapi
9	21	100.0	100000	9	AF000120	Homo sapi
10	21	100.0	100000	9	AF000120	Homo sapi
11	19.4	92.4	215	4	AF1329636	Sequence
12	19.4	92.4	225	4	AF079211	Sub scrof
13	19.4	92.4	732	6	AX0406943	Sequence
14	19.4	92.4	732	6	AX0406945	Sequence
15	19.4	92.4	117120	2	AC096260	Rattus no
16	18.4	87.6	192531	5	AL772193	Zebrafish
17	18.4	87.6	217073	2	AC094162	Rattus no
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19	18	85.7	91175	2	AF003758	Pyiza sat
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21	17.8	84.8	372	10	AY050513	Cavia por
22	17.8	84.8	468	10	AF071003	Rattus no
23	17.8	84.8	1664	10	BC022659	Mus muscu
24	17.8	84.8	2172	4	ECA292081	Equus cab
25	17.8	84.8	3883	5	AF428143	Salmo sal
26	17.8	84.8	193205	2	AC110430	Rattus no
27	17.8	84.8	193205	2	AC110430	Rattus no
28	17.8	84.8	141726	2	AC110386	Rattus no
29	17.8	84.8	144709	2	AC117904	Rattus no
30	17.8	84.8	156140	9	AC067745	Homo sapi
31	17.8	84.8	174073	2	AC107534	Rattus no
32	17.8	84.8	186526	10	AU596083	Mouse DNA
33	17.8	84.8	215467	2	AC013420	Homo sapi
34	17.8	84.8	215467	2	AC013420	Homo sapi
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40	17.4	82.9	1302	14	AF222626	Influenza
41	17.4	82.9	2027	14	AF046086	Influenza
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ALIGNMENTS

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LOCUS	AX0406939	Sequence 1 from Patent WO022875.				
DEFINITION	AX0406939	Sequence 1 from Patent WO022875.				
ACCESSION	AX0406939	Sequence 1 from Patent WO022875.				
VERSION	AX0406939.1	GI:21439814				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Human sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Goldstein.S.A.					
TITLE	Polymorphisms associated with cardiac arrhythmia					
JOURNAL	Patent : WO 0222875-A 1 21-MAR-2002;					

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DEFINITION            Sequence 3 from Patent WO0222875.
ACCESSION              AX406941
VERSION                AX406941.1 GI:21439816
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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BASE COUNT          221 a 152 c 157 g 202 t
ORIGIN
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Db 230 CTCATGGTGATGATGGAATG 250

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LOCUS                 AX406947             732 bp    DNA        PAT 14-JUN-2002
DEFINITION            Sequence 9 from Patent WO0222875.
ACCESSION              AX406947
VERSION                AX406947.1 GI:21439817
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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Best Local Similarity 100.0%; Pred. No. 5.8;
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Db 230 CTCATGGTGATGATGGAATG 250

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DEFINITION            Hs. lens mink-related peptide 1 mRNA, complete cds.
ACCESSION              AF071002
VERSION                AF071002.1 GI:4704422
KEYWORDS
SOURCE                 Homo sapiens.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Abbott,G.W., Sesti,P., Buck,M.E., Lehmann,M.H.,
Timothy,K.W., Keating,M.T. and Goldstein,S.A.
TITLES                 MIRP1 forms IKr potassing channels with HERG and is associated with
cardiac arrhythmia
JOURNAL                Cell 97 (2), 175-187 (1999)
MEDLINE               99235979
PMID                  10522896
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Db 230 CTCATGGTGATGATGGAATG 250

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LOCUS                 AF071002             732 bp    mRNA       PRI 29-APR-1999
DEFINITION            Hs. lens mink-related peptide 1 mRNA, complete cds.
ACCESSION              AF071002
VERSION                AF071002.1 GI:4704422
KEYWORDS
SOURCE                 Homo sapiens.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Abbott,G.W., Sesti,P., Buck,M.E., Lehmann,M.H.,
Timothy,K.W., Keating,M.T. and Goldstein,S.A.
TITLES                 MIRP1 forms IKr potassing channels with HERG and is associated with
cardiac arrhythmia
JOURNAL                Cell 97 (2), 175-187 (1999)
MEDLINE               99235979
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BASE COUNT          219 a 152 c 159 g 202 t
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Best Local Similarity 100.0%; Pred. No. 5.8;
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DEFINITION            Sequence 9 from Patent WO0222875.
ACCESSION              AX406947
VERSION                AX406947.1 GI:21439817
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.8;
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DEFINITION            Sequence 9 from Patent WO0222875.
ACCESSION              AX406947
VERSION                AX406947.1 GI:21439817
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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ACCESSION            AX406947
VERSION              AX406947.1 GI:21439822
KEYWORDS
SOURCE               human.
ORGANISM             Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            1
AUTHORS              Goldstein,S.A.
TITLES               Polymorphisms associated with cardiac arrhythmia
JOURNAL              Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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Db 230 CTCATGGTGATGATGGAATG 250

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LOCUS                 AF071002             732 bp    mRNA       PRI 29-APR-1999
DEFINITION            Hs. lens mink-related peptide 1 mRNA, complete cds.
ACCESSION              AF071002
VERSION                AF071002.1 GI:4704422
KEYWORDS
SOURCE                 Homo sapiens.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Abbott,G.W., Sesti,P., Buck,M.E., Lehmann,M.H.,
Timothy,K.W., Keating,M.T. and Goldstein,S.A.
TITLES                 MIRP1 forms IKr potassing channels with HERG and is associated with
cardiac arrhythmia
JOURNAL                Cell 97 (2), 175-187 (1999)
MEDLINE               99235979
PMID                  10522896
BASE COUNT          219 a 152 c 159 g 202 t
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Query Match          100.0%; Score 21; DB 6; Length 732;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS                 AF071002             732 bp    mRNA       PRI 29-APR-1999
DEFINITION            Hs. lens mink-related peptide 1 mRNA, complete cds.
ACCESSION              AF071002
VERSION                AF071002.1 GI:4704422
KEYWORDS
SOURCE                 Homo sapiens.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Abbott,G.W., Sesti,P., Buck,M.E., Lehmann,M.H.,
Timothy,K.W., Keating,M.T. and Goldstein,S.A.
TITLES                 MIRP1 forms IKr potassing channels with HERG and is associated with
cardiac arrhythmia
JOURNAL                Cell 97 (2), 175-187 (1999)
MEDLINE               99235979
PMID                  10522896
BASE COUNT          219 a 152 c 159 g 202 t
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Query Match          100.0%; Score 21; DB 6; Length 732;
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RESULT 6
AX406947
LOCUS                 AX406947             732 bp    DNA        PAT 14-JUN-2002
DEFINITION            Sequence 9 from Patent WO0222875.
ACCESSION              AX406947
VERSION                AX406947.1 GI:21439817
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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Best Local Similarity 100.0%; Pred. No. 5.8;
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DEFINITION            Sequence 9 from Patent WO0222875.
ACCESSION              AX406947
VERSION                AX406947.1 GI:21439817
KEYWORDS
SOURCE                 human.
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE              1
AUTHORS                Goldstein,S.A.
TITLES                 Polymorphisms associated with cardiac arrhythmia
JOURNAL                Patent: WO 022875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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LOCUS      Homo sapiens voltage-gated K+ channel subunit MIRP1 (KCNE2) mRNA,
DEFINITION complete cds.
ACCESSION AF302095.1 GI:10121887
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 809)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Domenech, A., Bativill, X. and de la Luna, S.
TITLE      Cloning of human MIRP1 cDNA
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 809)
Domenech, A., Bativill, X. and de la Luna, S.
Direct Submission
GenBank accession number AF302095
INSTITUTION Institut Recerca Oncologica, Avda de Castelldefels km 2,7,
L'Hospital de Llobregat, Barcelona 08907, Spain
JOURNAL    Location/Qualifiers
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BASE COUNT      247 a 172 c 189 g 200 t 1 others
ORIGIN
Query Match      100.0%; Score 21; DB 9; Length 809;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATGGAATG 21
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Db 297 CTCATGGTGATGATGGAATG 317

RESULT 6
AF000320 24608 bp DNA linear PRI 20-NOV-1999
LOCUS      Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AM, region,
DEFINITION clone:Q12C8, complete sequence.
ACCESSION AP000320.1 GI:4835689
KEYWORDS
SOURCE      Homo sapiens DNA, clone:Q12C8.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 24608)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
TITLE      Homo sapiens 24,608bp genomic DNA of 21q22.1
JOURNAL    Published Only in Database (1999)
REFERENCE   2 (bases 1 to 24608)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Direct Submission
GenBank accession number AF000320
INSTITUTION Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hpg.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
JOURNAL    The sequence is a part of the data (ACCESSION No. AF000165 -
AP000173).
COMMENT     The sequencing project is supported by Japan Science Technology
Corporation (JST) and The Institute of Physical and Chemical
Research (RIKEN).
FEATURES
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BASE COUNT      6797 a 5420 c 5437 g 6954 t
ORIGIN
Query Match      100.0%; Score 21; DB 9; Length 24608;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATGGAATG 21
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Db 15852 CTCATGGTGATGATGGAATG 15872

RESULT 7
AP000052 10000 bp DNA linear PRI 20-NOV-1999
LOCUS      Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
DEFINITION complete sequence.
ACCESSION AP000052
KEYWORDS
SOURCE      Homo sapiens DNA, clone:245P17-64A4f_2.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 10000)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE      Homo sapiens genomic DNA, chromosome 21q
JOURNAL    Published Only in Database (1998)
REFERENCE   2 (bases 1 to 10000)
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Direct Submission
GenBank accession number AP000052
INSTITUTION Submitted (11-MAY-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
JOURNAL

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source	301583 CTCATGGTGATGATGGATG 301603 OY 1 CTCATGGTGATGATGGATG 21 Db 33 CTCATGGTGATGATGGATG 53 RESULT 12 LOCUS AY079211 DEFINITION SUB scrofa KCNE2 mRNA, partial cds. ACCESSION AY079211 VERSION AY079211.1 KEYWORDS SOURCE pig.
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source	

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Best Local Similarity   95.2%, Pred.No. 39;
Matches    20; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

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Db       230 CTCACGTGATGATGGAATG 250

RESULT 14
AC096240
LOCUS          AX406945
DEFINITION     Sequence 7 from Patent WO022875.
ACCESSION      AX406945
VERSION        AX406945.1 GI:21439820
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
Bukaryota; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
1
REFERENCE
AUTHORS        Goldstein,S.A.
TITLE          Polymorphisms associated with cardiac arrhythmia
JOURNAL        Parent: WO 022875-A 7 21-MAR-2002;
               YALE UNIVERSITY [US]
FEATURES       source
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                 /organism="Homo sapiens"
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Query Match          92.4%; Score 19.4; DB 6; Length 732;
Best Local Similarity 95.2%; Pred.No. 39;
Matches    20; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

QY      1 CTCATGGTGATGATGGAATG 21
Db       230 CTCATGGTGATGATGGAATG 250

RESULT 15
AC096240
DEFINITION     Rattus norvegicus clone CH220-78012, *** SEQUENCING IN PROGRESS
ACCESSION      AC096260
VERSION        AC096260.3 GI:21723414
KEYWORDS       HTG; HTGS PHASE1.
SOURCE         Norway rat.
Rattus norvegicus
Chordata; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentii; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 11720)
REFERENCE
AUTHORS        Murty,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
               Alebrooks,S.L., Amaratunga,H.C., Are,J.R., Ayele,M., Banks,T.,
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               Bouck,A., Bowie,S., Breiva,M., Brown,E., Brown,M., Bryant,N.P.,
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Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 bases 1 to 117120
W. bases 1 to 117120

Direct Submission
Unpublished
2 bases 1 to 117120
W. bases 1 to 117120

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Morley,K.C.

Direct Submission
Unpublished
2 bases 1 to 117120
W. bases 1 to 117120

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 10, 2002 this sequence version replaced gi:17943956.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Contact: hgc@bcm.tmc.edu/
Contact: hgc-help@bcm.tmc.edu
----- Project Information
Center project name: G5UJ
Center clone name: CH210-78012
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly: Phred; Phrap; Pilon; 99.33%
Consensus quality: 76897 bases at least Q40
Consensus quality: 76882 bases at least Q30
Consensus quality: 18184 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a working draft sequence. It currently
* contains gaps between the contigs. The gaps are
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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* be preserved.

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1
1481: contig of 1481 bp in length
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52447: gap of unknown length
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56288: gap of unknown length

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Query Match          92.4%; Score 19.4; DB 2; Length 117120;
Best Local Similarity 95.2%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 CTCATGCGATGATGCGATG 21
Db 70138 CTCATGCGATGATGCGATG 70158

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Search completed: June 9, 2003, 09:12:03
Job time : 605 secs

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GenScan version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 08:36:49 ; Search time 119 Seconds
(without alignments)
397.411 Million cell updates/sec

Title: US-09-550-163-1_COPY_230_250

Perfect score: 21

Sequence: 1 ccatggtgatcggaatg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2186239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	312	22	Human breast cell
2	21	100.0	312	22	Human breast cell
3	21	100.0	312	22	Human breast cell
4	21	100.0	312	22	Human breast cell
5	21	100.0	312	22	Human breast cell
6	21	100.0	312	22	Human breast cell
7	21	100.0	312	22	Human breast cell
8	21	100.0	312	22	Human breast cell
9	21	100.0	312	22	Human breast cell

10	21	100.0	372	22	AA174432
11	21	100.0	372	22	AA174432
12	21	100.0	372	22	AA174432
13	21	100.0	450	22	AA174432
14	21	100.0	450	22	AA174432
15	21	100.0	450	22	AA174432
16	21	100.0	450	22	AA174432
17	21	100.0	450	22	AA174432
18	21	100.0	450	22	AA174432
19	21	100.0	450	22	AA174432
20	21	100.0	450	22	AA174432
21	21	100.0	450	22	AA174432
22	21	100.0	471	22	AA174432
23	21	100.0	471	22	AA174432
24	21	100.0	471	22	AA174432
25	21	100.0	600	22	AA174432
26	21	100.0	600	22	AA174432
27	21	100.0	655	22	AA174432
28	21	100.0	732	21	AA174432
29	21	100.0	732	21	AA174432
30	21	100.0	732	21	AA174432
31	21	100.0	732	21	AA174432
32	21	100.0	732	21	AA174432
33	21	100.0	732	21	AA174432
34	21	100.0	732	21	AA174432
35	19.4	92.4	732	21	AA174432
36	19.4	92.4	732	21	AA174432
37	19.4	92.4	732	21	AA174432
38	19.4	92.4	732	21	AA174432
39	19.4	90.5	20	22	AA174432
40	17.8	84.8	65	24	AA174432
41	17.8	84.8	172	22	AA174432
42	16.8	80.0	583	22	AA174432
43	16.8	80.0	583	22	AA174432
44	16.8	80.0	583	22	AA174432
45	16.8	80.0	583	22	AA174432

ALIGNMENTS

RESULT 1
ABM49938
ID ABA49938 standard; DNA; 312 BP.

XX ABA49938;
XX AC ABA49938;
XX 01-FEB-2002 (first entry)
XX Human breast cell single exon nucleic acid probe #8633.
XX Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer; ss.
XX Homo sapiens.
XX W0200157271-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00662.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0208456.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.
 XX
 XX New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 XX
 XX Claim 4; SEQ ID NO 8633; 327bp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and/or 4% cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the
 CC hybridization signal. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression with far less bias
 CC than existing sequencing technologies. The invention is useful for
 CC identifying functional regions of genomic DNA. The invention is useful for
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WFO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 22; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCATGCGTGGATTCGATG 21
 Db 104 CTCATGCGTGGATTCGATG 124
 RESULT 2
 ID ABA67856 standard; DNA; 312 BP.
 XX ABA67856;
 XX
 XX ABA67856;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #1611.
 XX
 KM Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 XX Homo sapiens.
 XX
 PN W0200157277-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00669.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 XX
 XX 26-MAY-2000; 2000US-0207456.
 XX
 XX 30-JUN-2000; 2000US-0608408.
 XX
 XX 01-SEP-2000; 2000US-0234687.
 XX
 XX 21-SEP-2000; 2000US-0234687.
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 XX 27-SEP-2000; 2000US-0236359.
 XX
 XX 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 XX
 XX

PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX
 XX Claim 4; SEQ ID NO 16161; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC foetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WFO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 22; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCATGCGTGGATTCGATG 21
 Db 104 CTCATGCGTGGATTCGATG 124
 RESULT 3
 ID ABA34913 standard; DNA; 312 BP.
 XX ABA34913;
 XX
 XX ABA34913;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Probe #13379 for gene expression analysis in human heart cell sample.
 XX
 XX Human; gene expression; heart; microarray; vascular system; probe;
 XX cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease; ss.
 XX
 XX Homo sapiens.
 XX
 XX W0200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00666.
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 XX 04-FEB-2000; 2000US-0180312.
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 XX 26-MAY-2000; 2000US-0207456.
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 XX 30-JUN-2000; 2000US-0608408.
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 XX 01-SEP-2000; 2000US-0234687.
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 XX 21-SEP-2000; 2000US-0234687.
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 XX 27-SEP-2000; 2000US-0236359.
 XX
 XX 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488899/53.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts -
 PT
 PT Claim 4; SEQ ID No 13379; 530pp; English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 XX measuring human gene expression in a sample derived from human heart. The
 XX present sequence is one such probe. The probes may be used for
 XX predicting, measuring and displaying gene expression in samples derived
 XX from the human heart via microarrays. By measuring gene expression, the
 XX probes are useful for predicting, diagnosing, grading, staging.

KW Probe; human; microarray; gene expression; cervical epithelial cell;
 XX cervical cancer; ss.
 CS Homo sapiens.
 PN W0200157278-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00670.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 XX
 XX 26-MAY-2000; 2000US-0207456.
 XX
 XX 30-JUN-2000; 2000US-0609408.
 XX
 XX 03-AUG-2000; 2000US-0608408.
 XX
 XX 03-AUG-2000; 2000US-0632366.
 XX
 XX 21-SEP-2000; 2000US-0234687.
 XX
 XX 27-SEP-2000; 2000US-0236359.
 XX
 XX 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells -
 XX
 XX Claim 25; SEQ ID No 12706; 487bp; English.
 XX
 XX The present invention relates to human single exon nucleic acid probes
 XX (SENPs). The present sequence is one such probe. The SENPs are derived
 XX from human Hela cells. The SENPs can be used to produce a single exon
 XX microarray, which can be used for measuring human gene expression in a
 XX sample derived from human cervical epithelial cells. By measuring gene
 XX expression, the process of detecting and/or staging
 XX cervical cancer, including notably cervical cancer,
 XX can be improved.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
 XX
 XX Query Match 100.0%; Score 21; DB 22; Length 312;
 XX Best Local Similarity 100.0%; Pred. No. 1.9;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 CTCATGGTCGATGGGAATG 21
 XX 104 CTCATGGTCGATGGGAATG 124
 XX
 XX RESULT 7
 XX AAI48075
 XX ID AAI48075 standard; DNA; 312 BP.
 XX
 XX AC AAI48075;
 XX
 XX 17-OCT-2001 (first entry)
 XX
 XX Probe #16761 used to measure gene expression in human placenta sample.
 XX
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 XX genetic disorder; ss.
 XX
 XX Homo sapiens.
 XX
 XX W0200157272-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00663.
 XX
 XX Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -

PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0609408.
 PR 03-AUG-2000; 2000US-0608408.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 XX
 XX Claim 25; SEQ ID No 16761; 654bp; English.
 XX
 XX The present invention relates to single exon nucleic acid probes (SENPs).
 XX The present sequence is one such probe. The probes are useful for
 XX producing a microarray for predicting, measuring and displaying gene
 XX expression in samples derived from human placenta. The probes are useful
 XX for antenatal diagnosis of human genetic disorders.
 XX
 XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
 XX
 XX Query Match 100.0%; Score 21; DB 22; Length 312;
 XX Best Local Similarity 100.0%; Pred. No. 1.9;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 CTCATGGTCGATGGGAATG 21
 XX 104 CTCATGGTCGATGGGAATG 124
 XX
 XX RESULT 8
 XX AAI08446
 XX ID AAI08446 standard; DNA; 312 BP.
 XX
 XX AC AAI08446;
 XX
 XX 09-OCT-2001 (first entry)
 XX
 XX Probe #8437 used to measure gene expression in human breast sample.
 XX
 XX Probe; human; breast disease; breast cancer; development disorder; ss;
 XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 XX Homo sapiens.
 XX
 XX W0200157270-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US00661.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 XX
 XX 26-MAY-2000; 2000US-0207456.
 XX
 XX 30-JUN-2000; 2000US-0608408.
 XX
 XX 03-AUG-2000; 2000US-0632366.
 XX
 XX 21-SEP-2000; 2000US-0234687.
 XX
 XX 27-SEP-2000; 2000US-0236359.
 XX
 XX 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-476286/51.
 XX
 XX Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -

XX	Claim 25; SEQ ID No 8437; 322pp; English.
XX	
XX	The present invention relates to novel single exon nucleic acid probes.
XX	CC The present sequence is one such probe. The probes are useful for
XX	CC measuring human gene expression in a human breast sample, where the probe
XX	CC targets at high stringency to a nucleic acid expressed in the human
XX	CC breast. The probes are useful for the diagnosis, prognosis, grading,
XX	CC staging, monitoring and prognosing diseases of the human breast,
XX	CC particularly those diseases with polygenic aetiology. The disease
XX	CC include: breast cancer; disorders of development; inflammatory diseases
XX	CC of the breast; fibrocystic changes; proliferative breast disease and
XX	CC non-carcinoma tumours.
XX	CC Note: the sequence data for this patent did not form part of the printed
XX	CC record. The sequence data is available in electronic format directly from WIFO
XX	CC at ftp.wifo.int/pub/published_sequences .
XX	XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
XX	
XX	Query Match 100.0%; Score 21; DB 22; Length 312;
XX	Best Local Similarity 100.0%; Frad. No. 1.9;
XX	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1 CTCATGCTGATGATGGGAATG 21
DB	104 CTCATGGTGATGATGGGAATG 124
XX	
XX	RESULT 9
XX	XX ABS16039
XX	XX ID ABS16039 standard; DNA, 312 BP.
XX	XX
AC	XX ABS16039;
XX	
XX	19-AUG-2002 (first entry)
XX	
DE	Human genome-derived single exon probe ORF from lung SEQ ID No 16030.
XX	
XX	Human; sex: single exon probe; asthma; lung cancer; COPD; IID;
XX	XX chronic obstructive pulmonary disease; familial idiopathic disease;
XX	XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX	XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX	XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX	XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
XX	XX pulmonary aortic atherosclerosis; fibrocystic pulmonary dysplasia;
XX	XX primary ciliary dyskinesia; pulmonary hypertension;
XX	XX hyaline membrane disease; open reading frame; ORF.
XX	
OS	Homo sapiens.
XX	
XX	WO2001186003-A2.
XX	
PN	15-NOV-2001.
XX	
PD	30-JAN-2001; 2001WO-US00665.
XX	
PR	04-FEB-2000; 2000US-180312P.
XX	
PR	26-MAY-2000; 2000US-207456P.
XX	
PR	30-JUN-2000; 2000US-0608408.
XX	
PR	03-AUG-2000; 2000US-0632366.
XX	
PR	21-SEP-2000; 2000US-234687P.
XX	
PR	27-SEP-2000; 2000US-236359P.
XX	
PR	04-OCT-2000; 2000US-0024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPT; 2002-114183/15.
XX	
XX	Spatially-addressable set of single exon nucleic acid probes, used to
XX	XX measure gene expression in human lung samples -

PS Claim 4; SEQ ID NO 16030; 53app; English.

XX The invention relates to a spatially-addressable set of single exon
PS nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12187 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of a
CC nucleic acid probes, and a method for measuring gene expression in a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC (a) algorithmically predicting at least one exon from genomic sequences
CC labeled nucleic acids from eukaryotic mRNA, to identify a nucleic acid
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons belong to the same gene; identifying exons encoded by one
CC of 12011 sequences, mentioned in the specification or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC haemochromatosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karsagen syndrome, fibrocystic,
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe open reading frame of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC form from the GenBank database. The sequence data is available at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CTCATGTGGTGAATGGTGAATG 21
DB 104 CTCATGTGGTGAATGGTGAATG 124

RESULT 10
AA124432 standard; DNM, 372 BP.
AA124432 standard; DNM, 372 BP.
AA124432;
12-OCT-2001 (first entry)
Probe #14365 for gene expression analysis in human cervical cell sample.
Probe; human; microarray; gene expression; cervical epithelial cell;
cervical cancer; 66.
Homo sapiens.
MO200157278-A2.
09-AUG-2001.

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PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 05-MAR-2000; 2000US-0207456.
PR 10-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID No 14365; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human Hela cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC diseases of the cervix, thereby providing a method for early detection
CC of cervical cancer. The probe did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
Query Match 100.0%; Score 21; DB 22; Length 372;
Local Similarity 100.0%; Pred. No. 1; 0; 0; 0; 0; 0; 0; 0; 0; 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCATGGTGATGATGGAATG 21
DB 157 CTCATGGTGATGATGGAATG 177
Query Match 100.0%; Score 21; DB 22; Length 372;
Local Similarity 100.0%; Pred. No. 1; 0; 0; 0; 0; 0; 0; 0; 0; 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCATGGTGATGATGGAATG 21
DB 157 CTCATGGTGATGATGGAATG 177
RESULT 11
AA109965
ID AA109965 standard; DNA; 372 BP.
AC AA109965;
DT 09-OCT-2001 (first entry)
XX
XX Probe #9956 used to measure gene expression in human breast sample.
XX
XX Inflammatory disease; breast cancer; development disorder; ss;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
XX
XX WO2001157270-A2.
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 03-JUN-2000; 2000US-0608408.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
XX Claim 25; SEQ ID No 9956; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC These probes are useful for measuring human gene expression in a
CC hybridized at high stringency to a nucleic acid sample, where the probe
CC hybridizes at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC carcinoma of the breast.
CC
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
Query Match 100.0%; Score 21; DB 22; Length 372;
Local Similarity 100.0%; Pred. No. 1; 0; 0; 0; 0; 0; 0; 0; 0; 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCATGGTGATGATGGAATG 21
DB 157 CTCATGGTGATGATGGAATG 177
RESULT 12
AA500245
ID AA500245 standard; DNA; 372 BP.
AC AA500245;
DT 10-MAY-2001 (first entry)
XX
XX Human potassium channel regulatory protein, Mink2, DNA sequence.
XX
XX Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
XX angina; asthma; diabetes; renal insufficiency; urinary incontinence;
XX irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
XX
XX Homo sapiens.
XX
XX Key 1.372 Location/Qualifiers
XX CDS /*tag= a
XX /product= "MINK2 potassium channel protein"
XX
XX WO200114403-A1.
XX
XX 01-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-US22799.
XX
XX 20-AUG-1999; 99US-0379201.
XX
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX
XX Ficker E, Wible B, Brown AM;
XX WPI; 2001-218424/22.
XX P-PSDB; AAU00215.
XX
XX Novel potassium channel gene termed Mink2 encoding potassium channel
XX regulatory protein, useful for screening compounds that are useful for

```

PT treating diseases caused by aberrant potassium activity -
 XX Claim 1; Fig 9; 37pp; English.
 XX The sequence represents the coding sequence of human potassium channel
 CC regulatory protein, Mink2. Mink2 sequence is useful for producing a
 CC potassium channel regulatory protein useful for in vitro or in vivo
 CC screening of agonistic or antagonistic compounds that are useful for
 CC cardiorhythmia, epilepsy, and/or aberrant potassium activity, such as human
 CC cardiorhythmia, epilepsy, and/or aberrant potassium activity, such as human
 CC insufficiency, urinary incontinence, irritable colon, epilepsy,
 CC cerebrovascular ischaemia, and autoimmune disease.
 XX Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
 SQ Query Match 100.0%; Score 21; DB 22; Length 372;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCATGGTGATGATGGAATG 21
 Db 157 CTCATGGTGATGATGGAATG 177
 RESULT 13
 ABAA4797
 ID ABA44797 standard; DNA; 450 BP.
 XX ABA44797;
 XX 01-FEB-2002 (first entry)
 XX Human breast cell single exon nucleic acid probe #3492.
 XX Human; microarray; single exon probe; gene expression; breast;
 XX disease; cancer; es.
 XX Homo sapiens.
 XX WO200157271-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00662.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 03-JUN-2000; 2000US-0609408.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-496933/54.
 XX New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 XX Claim 1; SEQ ID NO 3492; 327pp + sequence listing; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for

CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the activity of a gene and
 CC data. The data of expression activity of a gene and data of gene
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIFO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 SQ Query Match 100.0%; Score 21; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCATGGTGATGATGGAATG 21
 Db 312 CTCATGGTGATGATGGAATG 332
 RESULT 14
 ABAS5252
 ID ABA55252 standard; DNA; 450 BP.
 XX ABA55252;
 XX 01-FEB-2002 (first entry)
 XX Human foetal liver single exon nucleic acid probe #3557.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe; es.
 XX Homo sapiens.
 XX WO200157277-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00669.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human foetal liver -
 XX Claim 1; SEQ ID NO 3557; 639pp + sequence listing; English.
 XX The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC foetal liver. The single exon nucleic acid probe of the invention
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIFO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 SQ

Search completed: June 9, 2003, 08:51:25
Job time : 120 secs

Query Match 100.0%; Score 21; DB 22; Length 450;
Best Local Similarity 100.0%; Pred.No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATTGGAATG 21
Db 312 CTCATGGTGATGATTGGAATG 332

RESULT 15

ABA24997

ID ABA24997 standard; DNA; 450 BP.

XX

XX ABA24997;

XX

XX 23-JAN-2002 (first entry)

XX

XX DE Probe #3463 for gene expression analysis in human heart cell sample.

XX

XX Human; gene expression; heart; microarray; vascular system; probe;

XX KW cardiovascular disease; hypertension; cardiac arrhythmia;

XX KW congenital heart disease; ss.

XX

XX OS Homo sapiens.

XX

XX PN NC0200157274-A2.

XX

XX PD 09-AUG-2001.

XX

XX PP 30-JAN-2001; 2001WO-US00666.

XX

XX PR 04-FEB-2000; 2000US-0180312.

XX PR

XX PR 26-MAY-2000; 2000US-0207456.

XX PR

XX PR 30-JUN-2000; 2000US-0608408.

XX PR

XX PR 03-AUG-2000; 2000US-0632366.

XX PR

XX PR 21-SEP-2000; 2000US-0234687.

XX PR

XX PR 27-SEP-2000; 2000US-0236353.

XX PR

XX PR 04-OCT-2000; 2000GB-0044483.

XX

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX XPI; 2001-48899/53.

XX

XX PT Single exon nucleic acid probes for analysing gene expression in human

XX PT hearts -

XX

XX PS Claim 1; SEQ ID No 3463: 530pp; English.

XX

XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC probes are useful for predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.

XX CC The sequence data for this patent did not form part of the printed
XX CC publication and is hereby incorporated by reference in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 450;

Best Local Similarity 100.0%; Pred.No. 2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATTGGAATG 21

Db 312 CTCATGGTGATGATTGGAATG 332

Result	No.	Score	Match	Query	DB	ID	Description
C	1	16.4	78.1	75002	4	US-08-961-527-48	Sequence 48, Appl
	2	16.2	77.1	1141	2	US-08-966-366-3	Sequence 3, Appl
	3	16.2	77.1	9495	1	US-08-921-819-1	Sequence 1, Appl
	4	16.2	77.1	9495	1	US-08-921-819-1	Sequence 1, Appl
C	5	15.8	77.1	19718	4	US-08-961-527-99	Sequence 99, Appl
	6	15.8	75.2	836	4	US-08-868-2074-180	Sequence 180, Appl
C	7	15.8	75.2	1569	2	US-08-933-772-1	Sequence 1, Appl
	8	15.8	75.2	1569	4	US-09-385-287-1	Sequence 1, Appl
	9	15.8	75.2	2013	4	US-09-423-890-3	Sequence 3, Appl
	10	15.8	75.2	2465	4	US-09-432-890-9	Sequence 9, Appl
	11	15.8	75.2	2503	3	US-08-461-1450-3	Sequence 3, Appl
	12	15.8	75.2	2503	1	US-08-472-934-11	Sequence 11, Appl
C	13	15.8	75.2	2503	2	US-08-333-4604-3	Sequence 3, Appl
	14	15.8	75.2	2503	2	US-08-461-146C-3	Sequence 1, Appl
	15	15.8	75.2	2503	2	US-08-461-146C-3	Sequence 1, Appl
	16	15.8	75.2	2503	3	US-08-461-1450-3	Sequence 3, Appl
	17	15.8	75.2	2503	3	US-08-461-1450-3	Sequence 11, Appl
	18	15.8	75.2	2503	3	US-08-461-1450-3	Sequence 5, Appl
C	19	15.8	75.2	2503	4	US-08-638-893-7	Sequence 7, Appl
	20	15.8	75.2	2503	6	5171604-1	Parent No. 5171604
	21	15.8	75.2	6911	1	US-08-311-174-4	Sequence 4, Appl
	22	15.8	75.2	7577	4	US-08-961-527-46	Sequence 46, Appl
C	23	15.2	72.4	399	4	US-09-641-638-45	Sequence 45, Appl
	24	15.2	72.4	519	4	US-09-134-001C-1235	Sequence 1235, Appl
	25	15.2	72.4	519	4	US-09-134-001C-1235	Sequence 1235, Appl
C	26	15.2	72.4	1084	2	US-08-194-009-110	Sequence 110, Appl
	27	15.2	72.4	1084	2	US-08-194-009-110	Sequence 110, Appl
	28	15.2	72.4	1084	2	US-08-408-356-110	Sequence 110, Appl

```
RESULT 2
; Sequence 3, Application US/0896316
; Patent No. 5932445 ON;
; GENERAL INFORMATION:
; APPLICANT: Lal Preeti
; APPLICANT: An-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; NUMBER OF SEQUENCES: 18
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; REGISTRATION NUMBER: 36,749
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; PRIORITY DATE: 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1141 base pairs
; TYPE: Coding
; STRANDEDNESS: Single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT15
; CLONE: 1682433
; US-08-966-316-3
; Query Match 77.1%; Score 16.7; DB 2; Length 1141;
; Best Local Similarity 85.7%; Pred. No. 74;
; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 CTCATGGTGCATGATGGATG 21
; Db 158 CTCATGGTGCATGATGGATG 178
;
; RESULT 3
; US-08-271-829-1
; Sequence 1, Application US/08271829
; Patent No. 5583021
; GENERAL INFORMATION:
; APPLICANT: William G. Dougherty and John A.
; APPLICANT: Richard J. Polley
; TITLE OF INVENTION: Production of Virus Resistant Plants
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Polley
; STREET: One World Trade Center
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10048
; COMPUTER READABLE FORM:
; REGISTRATION NUMBER: 36,749
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,829
; FILING DATE: February 19, 1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/838,509
; FILING DATE: February 19, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley, Esq.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: 245-40288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9495
; TYPE: Coding
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA to genomic RNA
; HYPOTHETICAL: No
; ANTI-SENSE: No N/A
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; ORGANISM: Tobacco Etch Virus (TEV)
; STRAIN: Highly Aphid Transmitted
; STRAIN:
; IMMEDIATE SOURCE: TEV propagated in
; IMMEDIATE SOURCE: N. tabacum Burley 49
; POSITION IN GENOME: N/A
; FEASIBILITY:
; NAME/KEY: Coat protein gene
; LOCATION: Genomic nucleotides 8518
; IDENTIFICATION METHOD: --
; OTHER INFORMATION: SEQ. ID NO. 5583021.1 is
; OTHER INFORMATION: the cDNA corresponding to the Tobacco
; OTHER INFORMATION: Etch Virus Genome.
; PUBLICATION INFORMATION:
; AUTHORS: Allison et al.
; TITLE: The nucleotide sequence of the
; TITLE: Genomic RNA: Evidence for the
; TITLE: Synthesis of a Single Polyprotein
; JOURNAL: Virology
; VOLUME: 154
; ISSUE: --
; PAGES: 9-20
; US-08-271-829-1
; Query Match 77.1%; Score 16.2; DB 1; Length 9495;
; Best Local Similarity 85.7%; Pred. No. 97;
; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 CTCATGGTGCATGATGGATG 21
; Db 7942 CTCATGGTGCATGATGGATG 7962
;
; RESULT 4
; PCT-US93-01544-1
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Sequence 1, Application PC/TUS9301544
GENERAL INFORMATION:
APPLICANT: William G. Dougherty and John A. Lindbo
TITLE OF INVENTION: Production of Plants Showing
TITLE OF INVENTION: Immunity to Viral Infection via Introduction of Genes
TITLE OF INVENTION: Encoding Untranslatable Plus Sense RNA Molecules
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Polley
STREET: 121 S.W. Salmon Street, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01544
FILING DATE: 19930218
CLASSIFICATION: DATA
PUBLICATION NUMBER:
FILING DATE: 19 PER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 245-35829/RJP
TELEPHONE: (503) 228-9441
TELEFAX: (503) 228-9441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9495
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULAR WEIGHT: 20850
DESCRIPTION: cDNA to genomic RNA
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: Tobacco Etch Virus (TEV)
STRAIN: Highly Aphid Transmitted (HAT)
IMMEDIATE SOURCE: BRL 49
POSITION IN GENOME: N/A
FEATURES:
NAME/KEY: Coat protein gene
LOCATION: Genomic nucleotides 8518-9306
IDENTIFICATION METHOD: --
OTHER INFORMATION: SEQ. ID NO. 1 is the cDNA
CORRESPONDING TO THE Tobacco Etch Virus Genome.
PUBLICATION INFORMATION:
AUTHORS: Allison et al.
TITLE: The nucleotide sequence of the coding
TITLE: region of Tobacco Etch Virus Genomic RNA:
TITLE: Evidence for the Synthesis of a Single
TITLE: Polyprotein
VOLUME: 154
ISSUE: --
PAGES: 9-20
PCT-US93-01544-1

Query Match 77.1%; Score 16.2; DB 5; Length 9495;
Best Local Similarity 85.7%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTTGATGATTGGAATG 21
Db 7942 CTTATGTTGATGATTGGAATG 7962

RESULT 5
US-08-961-527-99/c
Sequence 99, Application US/08961527
Patent No. 63481328
GENERAL INFORMATION:
APPLICANT: Charles Runsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340F1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 1971
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-99

Query Match 77.1%; Score 16.2; DB 4; Length 1971;
Best Local Similarity 85.7%; Pred. No. 114e-04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTTGATGATTGGAATG 21
Db 6079 CTTATGTTGATGATTGGAAG 6059

RESULT 6
US-08-958-207A-180/c
Sequence 180, Application US/08958207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Smedley, Robert
TITLE OF INVENTION: Sulfonamide Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

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/ COUNTRY: USA
/ ZIP: 19406-0919
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/858.207A
/ FILING DATE: 09-MAY-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 56/017670
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ginni, Edward R
/ REGISTRATION NUMBER: 38,891
/ REFERENCE/DOCKET NUMBER: P50475
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-4478
/ TELEFAX: 610-270-5090
/ INFORMATION FOR SEQ ID NO: 180:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 836 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-938-207A-180

Query Match 75.2%; Score 15.8; DB 4; Length 836;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCATGATGATGATGGAAT 20
DB 708 TCATGATGATGATGGAAT 690

RESULT 7
US-08-923-772-1/c
/ Sequence 1, Application US/08923772
/ Patent No. 1,59746510N
/ GENERAL INFORMATION:
/ APPLICANT: Black, Michael T.
/ TITLE OF INVENTION: NOVEL ffh
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: US
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/385.287
/ FILING DATE: 30-Aug-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/923,772
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dickinson, Todd Q
/ REGISTRATION NUMBER: 28,354
/ REFERENCE/DOCKET NUMBER: GM10080
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-994-2252
/ TELEFAX: 215-994-2222
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1569 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-09-385-287-1

Query Match 75.2%; Score 15.8; DB 4; Length 1569;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCATGATGATGATGGAAT 20
DB 316 TCATGATGATGATGGAAT 298

RESULT 8
US-09-385-287-1/c
/ Sequence 1, Application US/09385287
/ Patent No. 63309857
/ GENERAL INFORMATION:
/ APPLICANT: Black, Michael T.
/ TITLE OF INVENTION: NOVEL ffh
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: US
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/385.287
/ FILING DATE: 30-Aug-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/923,772
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dickinson, Todd Q
/ REGISTRATION NUMBER: 28,354
/ REFERENCE/DOCKET NUMBER: GM10080
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-994-2252
/ TELEFAX: 215-994-2222
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1569 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-09-385-287-1

Query Match 75.2%; Score 15.8; DB 4; Length 1569;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCATGATGATGATGGAAT 20
DB 316 TCATGATGATGATGGAAT 298

RESULT 9
US-09-423-890-3/c

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; Sequence 3, Application US/09423890
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CPT-085CPC
; CURRENT APPLICATION NUMBER: US/09/423,890
; PRIOR APPLICATION NUMBER: US/00/078,153
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: USSN 60/099,165
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3 013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(1980)
US-09-423-890-3

Query Match 75.2%; Score 15.8; DB 4; Length 2013;
Best Local Similarity 89.5%; Pred No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGGAA 19
Db 951 CTCCTGGTGATGAGAA 933

RESULT 10
US-09-423-890-3/c
; Sequence 9, Application US/09423890
; Patent No. 6312934
; GENERAL INFORMATION:
; APPLICANT: CADUS PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CPT-085CPC
; CURRENT APPLICATION NUMBER: US/09/423,890
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: USSN 60/078,153
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: USSN 60/099,165
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2465
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (427)..(2283)
US-09-423-890-9

Query Match 75.2%; Score 15.8; DB 4; Length 2465;
Best Local Similarity 89.5%; Pred No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGGAA 19
Db 1254 CTCCTGGTGATGAGAA 1236

RESULT 11
US-08-472-934-3/c
; Sequence 3, Application US/08472934
; Patent No. 5753446
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
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```
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
; FILE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive and Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/472,934
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,421
; FILING DATE: 15-May-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,516
; FILING DATE: 15-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,405,941
; FILING DATE: 15-Apr-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,460
; FILING DATE: 14-Oct-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11690
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04178
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Giulio A. DeConti, Jr. Esq.
; REGISTRATION NUMBER: 31,583
; REFERENCE TO OTHER PUBLICATIONS: CPT-004DVCF2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2503 base pairs
; TYPE: Nucleic acid
; STRATEGY: Genomic
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 466..2325
US-08-472-934-3

Query Match 75.2%; Score 15.8; DB 1; Length 2503;
Best Local Similarity 89.5%; Pred No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGGAA 19
Db 1293 CTCCTGGTGATGAGAA 1275

RESULT 12
US-08-472-934-11/c
; Sequence 11, Application US/08472934
; Patent No. 5753446
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
```

1 TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
2 NUMBER OF SEQUENCES: 12
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: LAHIVE AND COCKFIELD
5 STREET: 60 STATE STREET
6 STATE: MASSACHUSETTS
7 COUNTRY: U.S.A.
8 ZIP: 02109
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 CURRENT APPLICATION DATA: Release #1.0, Version #1.25
15 PRIORITY APPLICATION NUMBER: US/08/472,934
16 FILING DATE: 06-JUN-1995
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/440,421
20 FILING DATE: 15-APR-1993
21 PRIORITY APPLICATION NUMBER: 08/354,516
22 FILING DATE: 21-FEB-1995
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 5,405,941
25 FILING DATE: 15-APR-1993
26 PRIORITY APPLICATION NUMBER: 08/323,460
27 FILING DATE: 14-OCT-1994
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PCT/US94/11690
30 FILING DATE: 14-OCT-1994
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: PCT/US94/04178
33 FILING DATE: 15-APR-1994
34 NAME/KEY: CDS
35 LOCATION: 466..2325
36
37 TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
38 NUMBER OF SEQUENCES: 14
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE: LAHIVE AND COCKFIELD
41 STREET: 60 STATE STREET
42 STATE: MASSACHUSETTS
43 COUNTRY: U.S.A.
44 ZIP: 02109
45
46 COMPUTER READABLE FORM:
47 MEDIUM TYPE: Floppy disk
48 COMPUTER: IBM PC compatible
49 OPERATING SYSTEM: PC-DOS/MS-DOS
50 CURRENT APPLICATION DATA: Release #1.0, Version #1.25
51 PRIORITY APPLICATION NUMBER: US/08/461,146C
52 FILING DATE: 05-JUN-1995
53 CLASSIFICATION: 435
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 08/354,516

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: SHERIDAN ROSS & MCINTOSH
3 STREET: 1700 LINCOLN STREET, SUITE 3500
4 CITY: DENVER
5 STATE: CO USA
6 COUNTRY: U.S.A.
7 ZIP: 80203
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 CURRENT APPLICATION DATA: Release #1.0, Version #1.25
14 PRIORITY APPLICATION NUMBER: US/08/323,460A
15 FILING DATE: 14-OCT-1994
16 CLASSIFICATION: 530
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/049,254
19 FILING DATE: 14-APR-1993
20 ATTORNEY/AGENT INFORMATION:
21 NAME/KEY: CDS
22 LOCATION: 466..2325
23
24 TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
25 NUMBER OF SEQUENCES: 14
26 CORRESPONDENCE ADDRESS:
27 ADDRESSEE: LAHIVE AND COCKFIELD
28 STREET: 60 STATE STREET
29 STATE: MASSACHUSETTS
30 COUNTRY: U.S.A.
31 ZIP: 02109
32
33 COMPUTER READABLE FORM:
34 MEDIUM TYPE: Floppy disk
35 COMPUTER: IBM PC compatible
36 OPERATING SYSTEM: PC-DOS/MS-DOS
37 CURRENT APPLICATION DATA: Release #1.0, Version #1.25
38 PRIORITY APPLICATION NUMBER: US/08/461,146C
39 FILING DATE: 05-JUN-1995
40 CLASSIFICATION: 435
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: US 08/354,516

RESULT 14

US-08-461-146C-3/c
Sequence 3, Application US/08461146C

Patent No.5981265
GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.

TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive and Cockfield

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.25

PRIORITY APPLICATION NUMBER: US/08/461,146C

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/354,516

Query Match 75.2%; Score 15.8; DB 1; Length 2503;

Best Local Similarity 89.5%; Pred.No.1.3e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTCATGCGTATGATAGCAA 19

DB 1293 CTCCTGGTATGATAGCAA 1275

RESULT 13

US-08-323-460A-3/c

Sequence 3, Application US/08323460A

Patent No.5981265

GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.

TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL

RESPONSIVENESS TO EXTERNAL SIGNALS

NUMBER OF SEQUENCES: 10

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; FILING DATE: 21-FEB-1995
; PRIORITY/SEQUENCE: US 08/049,254
; APPLICATION NUMBER: 15-APR-1993
; FILING DATE: 15-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,460
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11690
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04178
; FILING DATE: 15-APR-1994
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41.106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 466..2325
; US-08-461-146C-3

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Best Local Similarity 89.5%; Pred No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCATGTCGATGATGGAA 19
Db 1293 CTCCTGTCGATGATGGAA 1275

RESULT 15
US-08-461-146C-11/c
; Sequence 11, Application US/08461146C
; Patent No. 5981265
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
; INVENTOR: JOHNSON, GARY L.
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lahive and Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: F
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,146C
; FILING DATE: 05-JUN-1995
; PRIORITY/SEQUENCE: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/354,516
; FILING DATE: 21-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,254
; FILING DATE: 15-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,460

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; FILING DATE: 14-OCT-1994
; PRIORITY/SEQUENCE: PCT/US94/11690
; APPLICATION NUMBER: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04178
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41.106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 466..2325
; US-08-461-146C-11

Query Match 75.2%; Score 15.8; DB 2; Length 2503;
Best Local Similarity 89.5%; Pred No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCATGTCGATGATGGAA 19
Db 1293 CTCCTGTCGATGATGGAA 1275

Search completed: June 9, 2003, 11:07:52
Job time : 43.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 09:12:21 : Search time 59.5 Seconds

(without alignments)

439,394 Million cell updates/sec

Title: US-09-550-163-1_COPY_230_250

Perfect score: 21

Sequence: 1 ctcattggtgatggatggaatg 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 69976693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/prodata/1/pubnpa/US06_PUBCOMB.seq:*

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14: /cgn2_6/prodata/1/pubnpa/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	21	100.0	471	10	US-09-864-761-20233
4	21	100.0	471	10	US-09-864-761-16671
5	21	100.0	732	9	US-10-009-151B-5
6	21	100.0	113604	9	US-10-227-195A-1
7	21	100.0	113604	9	US-10-227-195A-2
8	16.8	80.0	583	10	US-09-864-761-20772
9	16.8	80.0	707	9	US-10-011-585A-78
10	16.4	78.1	1320	10	US-09-864-761-012
11	16.4	78.1	1448	9	US-09-774-639-43
12	16.4	78.1	1448	9	US-09-969-730-52
13	16.4	78.1	1448	9	US-09-969-730-52
14	16.2	77.1	227	10	US-09-294-0938-5363
15	16.2	77.1	481	9	US-09-968-433-26
16	16.2	77.1	574	10	US-09-864-761-12791
17	16.2	77.1	1141	9	US-09-968-433-3
18	16.2	77.1	1653	10	US-09-529-063-80
19	16.2	77.1	2000	10	US-09-529-063-80

20	16.2	77.1	96649	9	US-09-956-712-10
21	16.2	77.1	96649	9	US-09-956-712-10
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23	15.8	75.2	257	10	US-09-878-574-7121
24	15.8	75.2	271	10	US-09-878-574-7121
25	15.8	75.2	382	10	US-09-878-574-7121
26	15.8	75.2	774	10	US-09-770-445-898
27	15.8	75.2	795	9	US-09-822-846-314
28	15.8	75.2	1339	9	US-09-728-546-2905
29	15.8	75.2	1339	9	US-09-728-546-2905
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35	15.8	75.2	2465	12	US-10-000-864-3
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41	15.2	72.4	213	10	US-09-864-761-29571
42	15.2	72.4	260	10	US-09-878-574-6372
43	15.2	72.4	335	9	US-09-782-974C-53
44	15.2	72.4	340	9	US-09-984-130-106
45	15.2	72.4	346	10	US-09-878-574-3002

ALIGNMENTS

RESULT 1
US-09-864-761-20233
Patent No. US20020048763A1
GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chem, Wensheng

TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Acemica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-06

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

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? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annonex Sequence Listing Engine vers. 1.1
? SEQ ID NO 20233
? LENGTH: 312
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AP00052.1
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
? OTHER INFORMATION: EXPRESSED IN HUMAN TISSUE, SIGNAL = 1.4
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? OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
? OTHER INFORMATION: EST_HUMAN HIT: A1246239.1, EVALUOE 0.00e+00
? OTHER INFORMATION: EST_HUMAN HIT: A1246239.1, EVALUOE 0.00e+00
? OTHER INFORMATION: SWISSPROT HIT: P91606, EVALUOE 3.00e-55
? OTHER INFORMATION: NT HIT: AF302095.1, EVALUOE 0.00e+00
? OTHER INFORMATION: NT HIT: g111526220, EVALUOE 0.00e+00
US-09-864-761-20233

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Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCATGCTGATGATTCGAATG 21
Db 104 CTCATGCTGATGATTCGAATG 124

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RESULT 2
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? Sequence 3139: Application US/09864761
? General Information:
? APPLICANT: Penn, Sharron G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? APPLICANT: Chen, Wensheng
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
? FILE DESCRIPTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: US/09/864,761
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: GB 24263.6
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? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665

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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
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? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
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? SEQ ID NO 3139
? LENGTH: 312
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AP000120.1
? OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.98
? OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 0.67
? OTHER INFORMATION: EST_HUMAN HIT: A163454, EVALUOE 0.00e-00
? OTHER INFORMATION: SWISSPROT HIT: P91606, EVALUOE 3.00e-57
? OTHER INFORMATION: NT HIT: g111526220, EVALUOE 0.00e+00
US-09-864-761-33139

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Query Match 100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCATGCTGATGATTCGAATG 21
Db 157 CTCATGCTGATGATTCGAATG 177

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RESULT 3
US-09-864-761-3463
? Sequence 3463: Application US/09864761
? General Information:
? APPLICANT: Penn, Sharron G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? APPLICANT: Chen, Wensheng
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
? FILE DESCRIPTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: US/09/864,761
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-08-03
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? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
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? PRIOR APPLICATION NUMBER: PCT/US01/00667
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? PRIOR APPLICATION NUMBER: PCT/US01/00664
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? PRIOR FILING DATE: 2001-01-30

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, PRIOR APPLICATION NUMBER: PCT/US01/00665
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, PRIOR APPLICATION NUMBER: US 09/774,203
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, OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
, OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
, OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
, OTHER INFORMATION: EXPRESSED IN FETAL TISSUE, SIGNAL = 1.1
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88
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US-09-864-761-3463

Query Match 100.0%; Score 21; DB 10; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 312 CTCATGGTGATGATGGGAATG 332

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US-864-761-16671
, Sequence 5, Application US/09864761
, Publication No. US20020048763A1
, APPLICANT: Penn, Sharron G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wenheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
, FILE REFERENCE: Vanderbilt Ref No. US2003001336A1
, CURRENT FILING DATE: 2000-10-30
, NUMBER OF SEQ ID NOS: 5
, SOFTWARE: GenBank Sequence Listing Engine vers. 1.1
, SEQ ID NO 5
, LENGTH: 732
, TYPE: DNA
, ORGANISM: Homo sapiens
, OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67
US-09-864-761-16671

Query Match 100.0%; Score 21; DB 9; Length 732;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATGGGAATG 21
Db 230 CTCATGGTGATGATGGGAATG 250

RESULT 5
US-10-000-151B-5
, Sequence 5, Application US/10000151B
, Publication No. US2003001336A1
, APPLICANT: Balcer, Jeffrey R.
, APPLICANT: George, Alfred L.
, TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
, FILE REFERENCE: Vanderbilt Ref No. US2003001336A1
, CURRENT FILING DATE: 2000-10-30
, NUMBER OF SEQ ID NOS: 5
, SOFTWARE: GenBank Sequence Listing Engine vers. 1.1
, SEQ ID NO 5
, LENGTH: 732
, TYPE: DNA
, ORGANISM: Homo sapiens
, OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67
US-09-864-761-16671

Query Match 100.0%; Score 21; DB 10; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATGGGAATG 21
Db 395 CTCATGGTGATGATGGGAATG 415

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US-10-000-151B-5
, Sequence 5, Application US/10000151B
, Publication No. US2003001336A1
, APPLICANT: Balcer, Jeffrey R.
, APPLICANT: George, Alfred L.
, TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
, FILE REFERENCE: Vanderbilt Ref No. US2003001336A1
, CURRENT FILING DATE: 2000-10-30
, NUMBER OF SEQ ID NOS: 5
, SOFTWARE: GenBank Sequence Listing Engine vers. 1.1
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, ORGANISM: Homo sapiens
, OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67
US-09-864-761-16671

Query Match 100.0%; Score 21; DB 9; Length 732;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCATGGTGATGATGGGAATG 21
Db 230 CTCATGGTGATGATGGGAATG 250

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RESULT 6
US-10-227-195A-1
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103J01
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: 757204..36973, 66372, 76921, 81512, 88727
; OTHER INFORMATION: n = G or C
US-10-227-195A-1

Query Match      100.0%; Score 21; DB 9; Length 113604;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

Qy      1  CTCATGCGTGATGATGGGAATG 21
Db      17632 CTCATGCGTGATGATGGGAATG 17652

RESULT 7
US-10-227-195A-2
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103J01
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
US-10-227-195A-2

Query Match      100.0%; Score 21; DB 9; Length 113604;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

Qy      1  CTCATGCGTGATGATGGGAATG 21
Db      17632 CTCATGCGTGATGATGGGAATG 17652

RESULT 8
US-09-864-761-20772
; Sequence 20772, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmice-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761

```

```

; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonex Sequence Listing Engine vers. 1.1
; SEQ ID NO 20772
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MAP TO AL022334.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEP2, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEPG2, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EST_HUMAN HIT: AW992395.1, EVALUE 9.50e-02
US-09-864-761-20772

Query Match      80.0%; Score 16.9; DB 10; Length 583;
Best Local Similarity 90.0%; Pred. No. 9e-02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  CTCATGCGTGATGATGGGAATG 21
Db      31  TCATGCGTGATGATGGGAATG 50

RESULT 9
US-10-011-585A-78
; Sequence 78, Application US/10011585A
; Publication No. US2003003986A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming

```


US-09-969-730-52

Query Match 78.1%; Score 16.4; DB 9; Length 1448;
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCATGCGATGATGGAA 19
 |||||
 Db 1094 TCATGCGATGATGGAA 1111

RESULT 14

US-09-294-0938-5363/C
 ; Sequence 5363, Application US/09294093B
 ; Patent No. US20010051335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ito, Tetsuhide, Raghunath, V.
 ; APPLICANT: Sherman, Bradley, K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 ; FILE REFERENCE: PL-0009 US
 ; CURRENT APPLICATION NUMBER: US/09/294,093B
 ; CURRENT FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: 60/082,567
 ; PRIORITY FILING DATE: April 21, 1998
 ; NUMBER OF SEQ ID NOS: 6207
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5363
 ; LENGTH: 227
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE: misc feature
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20010051335A1 700356460H1
 ; NAME/KEY: unshare
 ; LOCATION: 195, 206
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-294-0938-5363

Query Match 77.1%; Score 16.2; DB 10; Length 227;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTCATGCGATGATGGGAATG 21
 |||||
 Db 193 CTCATGCGATGATGGGAATG 173

RESULT 15

US-09-968-433-26
 ; Sequence 26, Application US/09968433
 ; Publication No. US20030073162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Murty, Lynn E.
 ; APPLICANT: Murty, M. N. S. R.
 ; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
 ; FILE REFERENCE: PC-0051 CIP
 ; CURRENT APPLICATION NUMBER: US/09/968,433
 ; CURRENT FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 26
 ; LENGTH: 481
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_Feature
 ; OTHER INFORMATION: Incyte ID No. US20030073162A1 2444714F6
 US-09-968-433-26

Query Match 77.1%; Score 16.2; DB 9; Length 481;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTCATGCGATGATGGGAATG 21
 |||||
 Db 158 CTCATGCGATGATGGGAATG 178

Search completed: June 9, 2003, 12:10:20
 Job time: 71.5 secs



Trace considered overall poor quality
Insert Length: 763 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

```
/clone_lib="SNO067"
/dev_stage="Adult"
/notes="Organ: stomach_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
from the stomach of adult rats. The cloning reaction
was performed under the following conditions:
NotI 196.716 - lundig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      60 a      80 c      76 g      95 t
ORIGIN
      1 CTCTGTCGTCGATTCGGAATG 21
      25 CTCTGTCGTCGATTCGGAATG 45
```

```
BASE COUNT      33 a      31 c      28 g      29 t
ORIGIN
      1 CTCTGTCGTCGATTCGGAATG 21
      5 CTCTGTCGTCGATTCGGAATG 25
```

```
RESULT 2
AM869303
LOCUS      AM869303      311 bp      mRNA      linear      EST 22-MAY-2000
DEFINITION      MKN-SNO067-24040-006-fill SNO067 Homo sapiens cDNA, mRNA sequence.
ACCESSION      AM869303.1
VERSION      AM869303.1 GI:8003356
KEYWORDS      EST.
SOURCE      human.
```

```
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto E, Garcia Correa R., Verjovski-Almeida S., Briones M.R.,
Nagai M.A., da Silva M.J., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.P., Matsukuma A., Baia G.S., Simpson D.H.,
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare
M.J., Soares P., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags.
Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
```

```
TITLE      Tral155-11-2704922
JOURNAL      Laboratory of Cancer Genetics
MEDLINE      Ludwig Institute for Cancer Research
COMMENT      Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil 55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=MR3-SNO067-240
400-006-f11c3=2000-04-24&c4=1)
Source: Ludwig Institute for Cancer Research
High quality sequence stop: 11
High quality sequence stop: 74.
```

FEATURES

source

```
/clone_lib="SNO067"
/dev_stage="Adult"
/notes="Organ: stomach_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
from the stomach of adult rats. The cloning reaction
was performed under the following conditions:
NotI 196.716 - lundig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      60 a      80 c      76 g      95 t
ORIGIN
      1 CTCTGTCGTCGATTCGGAATG 21
      25 CTCTGTCGTCGATTCGGAATG 45
```

```
BASE COUNT      60 a      80 c      76 g      95 t
ORIGIN
      1 CTCTGTCGTCGATTCGGAATG 21
      25 CTCTGTCGTCGATTCGGAATG 45
```

```
Query Match      100.0%; Score 21; DB 9; Length 311;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 CTCTGTCGTCGATTCGGAATG 21
Db      25 CTCTGTCGTCGATTCGGAATG 45
```

```
RESULT 3
AL1246239
LOCUS      AL1246239      372 bp      mRNA      linear      EST 28-JAN-1999
DEFINITION      g129g04.x1 Soares NHHPu_S1 Homo sapiens cDNA clone IMAGE:1857942
3' similar to SW-MINK HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
CHANNEL PROTEIN 1, mRNA sequence.
```

```
ACCESSION      AL1246239
VERSION      AL1246239.1 GI:1841636
KEYWORDS      EST.
SOURCE      human.
```

```
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 372)
National Center for Human Genome Research
National Center for Human Genome Research
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbsf-rcmail.nih.gov
```

```
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (http://imgb.nlm.nih.gov/) for further information.
1 (bases 1 to 372)
National Center for Human Genome Research
National Center for Human Genome Research
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbsf-rcmail.nih.gov
```

```
High quality sequence stop: 365.
Location/Qualifiers
1..372
```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="SNO067"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH108"
/notes="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
different libraries (metastatic melanoma, pregnant uterus,
and placenta) were digested with NotI and EcoRI and ligated
into the pT73D-Pac vector. The resulting recombinant
plasmids were transformed into DH108 cells and screened
for the presence of the expected insert. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260212-265223,
340486-345479, and 484488-489479."
```

```
BASE COUNT      115 a      89 c      86 g      82 t
ORIGIN
      1..311
Query Match      100.0%; Score 21; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


DNA sequencing by: Washington University Genome Sequencing Center
 Cloning distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.linn.gov/bbrp/image/Amegn.html
 Insert Length: 1077 bp Std Error: 0.00
 Seq. Percent: 100.00
 High quality sequence stop: 411.

FEATURES

Location/Qualifiers

1. .429
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2308895"
 /clone_lib="NCI-CGAP CGC"
 /lab_host="DH10B"
 /note="vector: pTR33-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI-CGAP GC4 was prepared, and
 as circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was FcH amplified cDNA from a pool
 of 1000 cells. The driver was then ligated into the pool
 1257098-1258631, 1469064-1470983, and 1475592-1476743".
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 127 a 100 c 97 g 104 t 1 others

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 9; Length 429;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

FEATURES

Location/Qualifiers

100.0%; Score 21; DB 12; Length 803;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

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Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

FEATURES

Location/Qualifiers

100.0%; Score 21; DB 12; Length 803;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

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Query Match

Best Local Similarity

Matches

cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

FEATURES

Location/Qualifiers

100.0%; Score 21; DB 12; Length 803;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

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Query Match

Best Local Similarity

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Query Match

Best Local Similarity

Matches

Query Match

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Matches

Query Match

Best Local Similarity

Matches

Query Match

Best Local Similarity

Matches

Query Match

/db xref="taxon:4577"
/clone_lib="683 - 14 day immature embryo from Hake lab (HS)"

/tissue_type="embryo"
/dev_stage="14 days after pollination"
/lab_host="DH10B", Vector: pBKCMV (Stratagene's Zap Express) Site 1: XhoI; Site 2: EcoRI; Directionally cloned. 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."
BASE COUNT 121 a 131 c 146 g 143 t
ORGANISM Zea mays. 1 others

Query Match 87.6%; Score 18.4; DB 10; Length 542;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCATGCTGATGATGGAATG 21
Db 132 TCATGCTGATGATGGAATG 113

RESULT 11
AM091474/c
LOCUS AM091474 579 bp mRNA linear EST 18-OCT-1999
DEFINITION 683028H09.x1 683 - 14 day immature embryo from Hake lab (HS) Zea mays cDNA, mRNA sequence.

ACCESSION AM091474
VERSION AM091474.1 GI:6057069
KEYWORDS Zea mays.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 579)
AUTHORS Walbot, ESTs from various cDNA libraries sequenced at Stanford University
TITLE Walbot, ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave. Palo Alto, CA 94304, USA
Fax: 650 725 4221
Email: walbot@stanford.edu
Plate: 683028 row: H column: 09.
Location/Qualifiers

FEATURES
source
1..579
/organism="Zea mays"
/cultivar="B73-4577"
/clone_lib="683 - 14 day immature embryo from Hake lab (HS)"
/tissue_type="embryo"
/dev_stage="14 days after pollination"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express) Site 1: XhoI; Site 2: EcoRI; Directionally cloned. 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."
BASE COUNT 119 a 150 c 167 g 143 t

Query Match 87.6%; Score 18.4; DB 10; Length 579;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCATGCTGATGATGGAATG 21
Db 107 TCATGCTGATGATGGAATG 88

RESULT 12
BN351227/c

LOCUS BN351227
DEFINITION M58275-A06.T3 ISUMS-RN Zea mays cDNA clone M58275-A06 3', mRNA
ACCESSION BN351227
VERSION BN351227.1 GI:18176183
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 595)
AUTHORS Men,T.J.; Qiu,F.; Guo,L.; Anhlock,D.A. and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Y. Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the Phred software,
http://dpcr.washington.edu/ventures/collabr/direct/index.htm#b73
The data were then analyzed using the Phred software (http://www.tigr.org/sofflab/s/).
Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
Location/Qualifiers

source
1..595
/organism="Zea mays"
/cultivar="B73-4577"
/clone_lib="M58275-A06"
/clone_lib="ISUMS-RN"
/tissue_type="mixed"
/lab_host="DH10B"
/note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI.
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), mixed mature tissues (30, 36, 41, 46, 51, 56, 61, 66, 71, 76, 81, 86, 91, 96, 101, 106, 111, 116, 121, 126, 131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186, 191, 196, 201, 206, 211, 216, 221, 226, 231, 236, 241, 246, 251, 256, 261, 266, 271, 276, 281, 286, 291, 296, 301, 306, 311, 316, 321, 326, 331, 336, 341, 346, 351, 356, 361, 366, 371, 376, 381, 386, 391, 396, 401, 406, 411, 416, 421, 426, 431, 436, 441, 446, 451, 456, 461, 466, 471, 476, 481, 486, 491, 496, 501, 506, 511, 516, 521, 526, 531, 536, 541, 546, 551, 556, 561, 566, 571, 576, 581, 586, 591, 596).
Tassel (1-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACP (alpha-chlorophenyl acid)-treated seedlings, Brassinolide-treated seedlings, ABA (abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'-ACACGAGAAATTCGCGCCGAGAAATTTTTTTTTTTT-3'). The resulting cDNA was then ligated with Phase H and used as template for DNA polymerase II catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library

then went through one round of normalization to CoT value
of 5 and then a second round of Maroto Benito Soares (Genome
Research 6: 791-806, 1996).
BASE COUNT 129 a 153 c 166 g 147 t

Query Match 87.6%; Score 18.4; DB 13; Length 595;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TCATGGTGATGATGGAATG 21
Db 125 TCATGGTGATGATGGAATG 106

RESULT 13
LOCUS AN076451/c 610 bp mRNA linear EST 14-OCT-1999
DEFINITION 683018E04.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
mays cDNA, mRNA sequence.
ACCESSION AN076451
VERSION
KEYWORDS EST.
ORGANISM Zea mays.

REFERENCE
AUTHORS Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 610)

Malbot.V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Department of Biological Sciences

Contact: Walbot V

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 725 8227

Fax: 650 725 8221

Email: walbot@stanford.edu

Place: 683018E04.x1 Column: 04.

Location/Qualifiers

1..610

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone_lib="683 - 14 day immature embryo from Hake lab (HS

/tissue_type="embryo"

/dev_stage="14 days after pollination"

/lab_host="DH10B"

/notes="Organ: embryo; Vector: pBKGW (Stratagene's Zap

/Express); Site 1: XhoI; Site 2: EcoRI; Directionally

cloned, 14 day immature embryo library created with

Stratagene's Zap Express cDNA protocol."

126 a 155 c 180 g 148 t 1 others

BASE COUNT

Query Match 87.6%; Score 18.4; DB 10; Length 610;

Best Local Similarity 95.0%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TCATGGTGATGATGGAATG 21

Db 107 TCATGGTGATGATGGAATG 88

RESULT 14
LOCUS AV702181 623 bp mRNA linear EST 08-OCT-2000
DEFINITION AV702181 ADB Homo sapiens cDNA clone ADBDA11 5', mRNA sequence.
VERSION AV702181.1 GI:10718511

KEYWORDS
SOURCE
ORGANISM

Human
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 623)

AUTHORS Peng Y., Song H., Huang Q., Huang C., Gu Y., Yang Y., Gao G., Xiao
H., Xu X., Li N., Qian B., Liu F., Qu J., Gao X., Cheng Z., Xu Z.,
Zeng L., Xu S., Gu M., Tu Y., Jia J., Fu G., Ren S., Zhong M., Lu
H., Chen Z. and Han Z.

TITLS Homo sapiens cDNA ADB clones

JOURNAL Unpublished (2000)

COMMENT Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801922 (ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..623

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="ADBDA11"

/tissue_type="Adrenal gland"

/dev_stage="Adult"

/lab_host="SOLR"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 171 a 112 c 115 g 217 t 8 others

ORIGIN

Query Match 87.6%; Score 18.4; DB 10; Length 623;

Best Local Similarity 95.0%; Pred. No. 5.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TCATGGTGATGATGGAATG 21

Db 554 TCATGGTGATGATGGAATG 573

RESULT 15
LOCUS BM351807/c 634 bp mRNA linear EST 16-JAN-2002
DEFINITION MEST346-G08.T3 ISUMS-RN Zea mays cDNA clone MEST346-G08 3', mRNA

sequence.

ACCESSION BM351807.1 GI:18176874

VERSION

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 634)

AUTHORS Wen Q., Guo L., Ashlock D.A. and Schnable P.S.

Expressed Sequence Tags from B73 Maize; various stages and tissues

including seedlings treated with a variety of hormones

Unpublished (2001)

JOURNAL Contact: Patrick S. Schnable

COMMENT Schnable Laboratory

Iowa State University

2405 S. Linn Drive, Ames, Iowa State University, Ames, IA 50011-1010, USA

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Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

phred software,

(<http://dept.washington.edu/ventures/collabr/direct/index.htm#b

rt). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/>).

C 247	14	7, 7	2801	4	US-09-005-051-30	Sequence 30, Appl	13	7, 2	320	17	3	US-09-265-628-18	Sequence 18, Appl
C 248	14	7, 7	2836	4	US-08-717-221B-24	Sequence 24, Appl	13	7, 2	321	17	4	US-09-101-41-16	Sequence 16, Appl
C 249	14	7, 7	2836	3	US-08-717-221B-24	Sequence 24, Appl	13	7, 2	322	17	4	US-09-101-41-16	Sequence 16, Appl
C 250	14	7, 7	2836	3	US-08-747-221B-26	Sequence 26, Appl	13	7, 2	323	17	4	US-09-523-217-76	Sequence 76, Appl
C 251	14	7, 7	2836	4	US-09-005-051-24	Sequence 24, Appl	13	7, 2	324	17	4	US-09-523-403-19	Sequence 19, Appl
C 252	14	7, 7	2836	4	US-09-005-051-26	Sequence 26, Appl	13	7, 2	325	17	4	US-09-284-531B-14	Sequence 14, Appl
C 253	14	7, 7	2885	4	US-09-232-200-36	Sequence 36, Appl	13	7, 2	326	17	4	US-09-434-408-11	Sequence 11, Appl
C 254	14	7, 7	2885	4	US-09-232-200-56	Sequence 56, Appl	13	7, 2	327	17	4	US-10-013-784-19	Sequence 19, Appl
C 255	14	7, 7	2885	4	US-09-232-197-36	Sequence 36, Appl	13	7, 2	328	17	5	PCR-0831-08174-1	Sequence 1, Appl
C 256	14	7, 7	2885	4	US-09-232-201-56	Sequence 56, Appl	13	7, 2	329	17	5	PCR-0831-08174-1	Sequence 1, Appl
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C 260	14	7, 7	3513	4	US-09-058-260-1	Sequence 1, Appl	13	7, 2	333	18	3	US-09-285-465-43	Sequence 43, Appl
C 261	14	7, 7	3545	4	US-08-781-802-9	Sequence 9, Appl	13	7, 2	334	18	3	US-09-287-710-6	Sequence 6, Appl
C 262	14	7, 7	3558	4	US-09-134-001C-2439	Sequence 2439, Ap	13	7, 2	335	18	3	US-08-621-700-11	Sequence 11, Appl
C 263	14	7, 7	3577	4	US-08-017-648-1	Sequence 1, Appl	13	7, 2	336	18	4	US-08-971-090-9	Sequence 9, Appl
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C 265	14	7, 7	3977	1	US-08-217-528-1	Sequence 1, Appl	13	7, 2	338	19	5	US-08-971-090-9	Sequence 9, Appl
C 266	14	7, 7	4315	4	US-08-781-802-1	Sequence 1, Appl	13	7, 2	339	20	1	US-09-509-565-21	Sequence 21, Appl
C 267	14	7, 7	4315	4	US-08-694-078-1	Sequence 1, Appl	13	7, 2	340	20	1	US-08-117-361C-9	Sequence 9, Appl
C 268	14	7, 7	4491	4	US-09-837-863-23	Sequence 23, Appl	13	7, 2	341	20	3	US-09-023-221A-17	Sequence 17, Appl
C 269	14	7, 7	4755	4	US-09-837-863-23	Sequence 23, Appl	13	7, 2	342	20	3	US-08-834-901-2	Sequence 2, Appl
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C 275	14	7, 7	5186	2	US-08-596-366-1	Sequence 1, Appl	13	7, 2	348	22	2	US-08-766-856A-2	Sequence 2, Appl
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C 277	14	7, 7	5253	3	US-08-714-918-19	Sequence 19, Appl	13	7, 2	350	22	4	US-08-870-180B-7	Sequence 7, Appl
C 278	14	7, 7	5253	4	US-09-265-315-19	Sequence 19, Appl	13	7, 2	351	22	4	US-09-226-529-7	Sequence 7, Appl
C 279	14	7, 7	5253	4	US-09-265-315-19	Sequence 19, Appl	13	7, 2	352	23	2	US-09-254-352B-13	Sequence 13, Appl
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C 284	14	7, 7	7559	2	US-08-250-548-2	Sequence 2, Appl	13	7, 2	357	23	3	US-08-958-201-20	Sequence 20, Appl
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C 292	14	7, 7	16355	4	US-08-961-527-74	Sequence 74, Appl	13	7, 2	365	24	1	US-07-910-867B-17	Sequence 17, Appl
C 293	14	7, 7	18436	4	US-08-961-527-87	Sequence 87, Appl	13	7, 2	366	24	1	US-08-488-212A-12	Sequence 12, Appl
C 294	14	7, 7	20137	4	US-09-263-773-206	Sequence 206, Appl	13	7, 2	367	24	1	US-08-387-845-7	Sequence 7, Appl
C 295	14	7, 7	20137	4	US-09-263-773-206	Sequence 206, Appl	13	7, 2	368	24	1	US-08-346-613-17	Sequence 17, Appl
C 296	14	7, 7	22011	4	US-08-263-773-210	Sequence 21, Appl	13	7, 2	369	24	1	US-08-476-562-50	Sequence 50, Appl
C 297	14	7, 7	22011	4	US-08-263-773-210	Sequence 21, Appl	13	7, 2	370	24	1	US-08-476-562-50	Sequence 50, Appl
C 298	14	7, 7	22011	4	US-08-961-527-48	Sequence 48, Appl	13	7, 2	371	24	1	US-08-479-723A-10	Sequence 10, Appl
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C 304	14	7, 7	45326	4	US-08-142-051-15	Sequence 15, Appl	13	7, 2	377	24	2	US-08-482-182-56	Sequence 56, Appl
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C 311	13	7, 2	17	1	US-08-113-026-13	Sequence 13, Appl	13	7, 2	384	24	2	US-08-461-965-101	Sequence 101, Appl
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C 314	13	7, 2	17	1	US-08-453-554-13	Sequence 1, Appl	13	7, 2	387	24	2	US-08-320-106-12	Sequence 12, Appl
C 315	13	7, 2	17	1	US-08-086-631-1	Sequence 1, Appl	13	7, 2	388	24	2	US-08-488-209B-12	Sequence 12, Appl
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C 318	13	7, 2	17	3	US-09-081-180-18	Sequence 18, Appl	13	7, 2	391	24	2	US-08-964-725-8	Sequence 8, Appl
C 319	13	7, 2	17	3	US-09-040-040-13	Sequence 13, Appl	13	7, 2	392	24	2	US-08-326-110A-14	Sequence 14, Appl
C 320	13	7, 2	17	3	US-09-040-040-13	Sequence 13, Appl	13	7, 2	393	24	2	US-08-975-527-6	Sequence 6, Appl

539	13	7, 2	160	1	US-08-327-525A-22	Sequence 22	Appl
540	13	7, 2	160	1	US-08-327-525A-23	Sequence 23	Appl
541	13	7, 2	160	1	US-08-337-525A-25	Sequence 25	Appl
542	13	7, 2	160	1	US-08-327-525A-26	Sequence 26	Appl
543	13	7, 2	160	1	US-08-327-525A-27	Sequence 27	Appl
544	13	7, 2	160	2	US-08-531-137B-19	Sequence 19	Appl
545	13	7, 2	160	2	US-08-531-137B-20	Sequence 20	Appl
546	13	7, 2	160	2	US-08-531-137B-21	Sequence 21	Appl
547	13	7, 2	160	2	US-08-531-137B-22	Sequence 22	Appl
548	13	7, 2	160	2	US-08-531-137B-25	Sequence 25	Appl
549	13	7, 2	160	2	US-08-531-137B-26	Sequence 26	Appl
550	13	7, 2	160	2	US-08-531-137B-27	Sequence 27	Appl
551	13	7, 2	160	4	US-09-158-765-19	Sequence 19	Appl
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556	13	7, 2	160	4	US-09-158-765-26	Sequence 26	Appl
557	13	7, 2	160	4	US-09-158-765-27	Sequence 27	Appl
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559	13	7, 2	161	2	US-09-073-674-15	Sequence 15	Appl
560	13	7, 2	162	2	US-09-332-542-22	Sequence 22	Appl
561	13	7, 2	165	2	US-08-757-663-49	Sequence 49	Appl
562	13	7, 2	165	4	US-08-520-946-49	Sequence 49	Appl
563	13	7, 2	165	4	US-08-520-946-49	Sequence 49	Appl
564	13	7, 2	173	4	US-09-025-76958-277	Sequence 277	Appl
565	13	7, 2	175	5	FCr-US93-06251-55	Sequence 55	Appl
566	13	7, 2	183	4	US-09-060-756-42	Sequence 42	Appl
567	13	7, 2	187	1	US-08-074-935-7	Sequence 7	Appl
568	13	7, 2	187	1	US-08-734-935-8	Sequence 8	Appl
569	13	7, 2	188	1	US-08-734-935-9	Sequence 9	Appl
570	13	7, 2	198	1	US-08-276-832-9	Sequence 9	Appl
571	13	7, 2	198	1	US-08-699-575-6	Sequence 6	Appl
572	13	7, 2	198	1	US-08-699-575-8	Sequence 8	Appl
573	13	7, 2	198	1	US-08-699-575-9	Sequence 9	Appl
574	13	7, 2	198	1	US-08-699-575-9	Sequence 9	Appl
575	13	7, 2	198	5	FCr-US95-08743-8	Sequence 8	Appl
576	13	7, 2	198	5	FCr-US95-08743-9	Sequence 9	Appl
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578	13	7, 2	201	1	US-08-732-832-41	Sequence 41	Appl
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580	13	7, 2	201	1	US-08-332-730A-114	Sequence 114	Appl
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ALIGNMENTS

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; Patent No. 5624791
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.311
; FILING DATE:
; CLASSIFICATION: 424
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; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C2
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; TELEPHONE: (904) 372-5800
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid

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; REFERENCE/DOCKET NUMBER: UF15.C3
; TELECOMMUNICATION INFORMATION:
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; SEQUENCE CHARACTERISTICS: 5:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; LOCATION: CDS
; ORIGIN: 374...1424
US-08-570-311-5
Query Match
Best Local Similarity 9.9%; Score 18; DB 1; Length 1841;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 GCTGCGAGAGCTCTTCGC 41
DB 1627 GCTGCGAGAGCTCTTCGC 1610
RESULT 2
US-08-353-485-5/c
; Sequence 5, Application US/0853485
; Patent No. 5624791
; GENERAL INFORMATION:
; APPLICANT: Proguiske-Fox, Ann
; APPLICANT: Tumwasorn, Somying
; APPLICANT: Lepine, Guylaine
; APPLICANT: Han, Naiming
; APPLICANT: Lantz, Marilyn
; APPLICANT: Patti, Joseph
; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ted W. Whitlock
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,485
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,119
; FILING DATE: 25-JAN-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/241,640
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF15.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 372-5800
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 374..1424
US-08-353-485-5
Query Match          9.9%; Score 18; DB 2; Length 1841;
Best Local Similarity 100.0%; Pred. No. 1.77;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      24  GCTGGAGAGCGTCTCCG 41
DB      1627 GCTGGAGAGCGTCTCCG 1610

RESULT 3
US-08-446-794A-3/C
; Sequence 3, Application US/08446794A
; Patent No. 5747327
; GENERAL INFORMATION:
; APPLICANT: UERI/NOVA, SWINI
; TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
; TITLE OF INVENTION: PLANT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA, USA
; COUNTRY: U.S.A.
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,794A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0760-0203P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2804 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..2542
US-08-446-794A-3
Query Match          9.9%; Score 18; DB 1; Length 2804;
Best Local Similarity 100.0%; Pred. No. 1.77;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      23  CCGTGGAGAGCGTCTCC 40
DB      2310 CCGTGGAGAGCGTCTCC 2293

RESULT 4
US-08-378-698-2/C
; Sequence 2, Application US/08378698
; Patent No. 576914
; GENERAL INFORMATION:
; APPLICANT: Delts, Thomas L.
; TITLE OF INVENTION: METHOD OF PRODUCING AND PURIFYING ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Delts, Thomas L. & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,698
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Delts, Thomas L.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 560336.90489
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2804 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-378-698-2
Query Match          9.4%; Score 17; DB 1; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      61  ATGGCAATTGGCGCCA 77
DB      63  ATGGCAATTGGCGCCA 47

RESULT 5
PCT-US96-00728-2/C
; Sequence 2, Application PC/TUS9600728
; GENERAL INFORMATION:
; APPLICANT: Delts, Thomas L.
; TITLE OF INVENTION: METHOD OF PRODUCING AND PURIFYING ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Delts, Thomas L. & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00728
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.

```

REGISTRATION NUMBER: 35 433
REFERENCE/DOCKET NUMBER: 560136.90489
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQUENCE NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-00728-2

Query Match 9.4%; Score 17; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 61 ATGGACAAATTGGCCCA 77
DB 63 ATGGACAAATTGGCCCA 47

RESULT 6
US-08-446-794A-3
Sequence 3, Application US/08446794A
GENERAL INFORMATION:
APPLICANT: Ueki, Jun
TITLE OF INVENTION: SHINJI
TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: P.O. BOX 747
CITY: FAIRFIELD
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/446,794A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
TELEPHONE: 703-205-8000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2804 base pairs
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 107..2542
US-08-446-794A-3

Query Match 9.4%; Score 17; DB 1; Length 2804;
Best Local Similarity 100.0%; Pred. No. 5.8; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 24 GCTGGAGACGCTCTCC 40
DB 2290 GCTGGAGACGCTCTCC 2306

RESULT 7
US-09-328-111-381/c
Sequence 381, Application US/09328111
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Biele, John
APPLICANT: Biele, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Nohadani, John E.
APPLICANT: Scharf, David
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
EARLIER FILING DATE: 1999-06-08
CURRENT FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 381
LENGTH: 622
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc-feature
LOCATION: (1)-(622)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-381

Query Match 8.8%; Score 16; DB 4; Length 622;
Best Local Similarity 100.0%; Pred. No. 19; 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 57 TTATATGGCAATTGG 72
DB 22 TTATATGGCAATTGG 7

RESULT 8
US-09-342-648-7/c
Sequence 648, Application US/09342648
GENERAL INFORMATION:
APPLICANT: Caboon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
TITLE OF INVENTION: PRODUCTS
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER FILING DATE: 1999-06-29
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 1626
TYPE: DNA
ORGANISM: Triticum aestivum
NAME/KEY: unseq
LOCATION: (1621)


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US-09-342-648-7
Query Match      8.8%; Score 16; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      85 ACAGCTGACCAAGG 100
DB      1166 ACAGCTGACCAAGG 1151

RESULT 9
US-08-975-080-35
; Sequence 35, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKTUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMMUNICATIONS RELEASE #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/975,080
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; FIRM: MORGAN, LEWIS & BOCKTUS LLP
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14796 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-975-080-35
Query Match      8.8%; Score 16; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      46 ATTATTATTACTTATA 61
DB      10809 ATTATTATTACTTATA 10824

RESULT 10
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION NUMBER: US/09/630,706

US-09-342-648-7
Query Match      8.8%; Score 16; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      85 ACAGCTGACCAAGG 100
DB      1166 ACAGCTGACCAAGG 1151

RESULT 9
US-08-975-080-35
; Sequence 35, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKTUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMMUNICATIONS RELEASE #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/975,080
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; FIRM: MORGAN, LEWIS & BOCKTUS LLP
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14796 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-975-080-35
Query Match      8.8%; Score 16; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      46 ATTATTATTACTTATA 61
DB      10809 ATTATTATTACTTATA 10824

RESULT 10
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION NUMBER: US/09/630,706

US-09-550-163-1_copy_80_260.oligo.rml
Query Match      8.8%; Score 16; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      46 ATTATTATTACTTATA 61
DB      10809 ATTATTATTACTTATA 10824

RESULT 12
US-09-221-017B-994
; Sequence 994, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
```

APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
DR. ROBERT L. JOHNSON & FORRSTER
FIRMING, INC.
STREET: 755 PINE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
REGISTRATION NUMBER: 27340-20021.00
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221.017B
FILING DATE: 23-DEC-1998

CLASSIFICATION:
PRIOR APPLICATION DATA: P01182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA: P01182
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: P01546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: P02911
FILING DATE: 10-DEC-1998
PRIOR APPLICATION DATA: P02911
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32.430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-8115600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 994:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
STRANDEDNESS: double
SOFTWARE: ASCII text
TOPOLOGY: circular
MOLSCULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE/KEY: misc feature
LOCATION: 1...797

US-09-221-017B-994
Query Match 8.3%; Score 15; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CCCTCCAGCCCAAG 115
Db 422 CCCTCCAGCCCAAG 436

RESULT 13 001C-1175
US-09-134-001C-1175
Best Local Similarity 100.0%; Pred. No. 67;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 TGATTTGAATGTTCT 175
Db 272 TGATTTGAATGTTCT 258

CURRENT APPLICATION NUMBER: US/09/134.001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-11-08 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1175
LENGTH: 1854
TYPE: DNA
ORGANISM: Staphylococcus epidermidie
US-09-134-001C-1175

Query Match 8.3%; Score 15; DB 4; Length 1854;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 GTACCTCATGTCAT 161
Db 1750 GTACCTCATGTCAT 1764

RESULT 14

US-08-961-527-174/c
Sequence 174, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
REGISTRATION NUMBER: 32.430
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 351
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 32.430
FILING DATE: 05/08/961,527
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kunch
REGISTRATION NUMBER: 33.373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-174
Query Match 8.3%; Score 15; DB 4; Length 2069;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 TGATTTGAATGTTCT 175
Db 272 TGATTTGAATGTTCT 258

APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
DR. ROBERT L. JOHNSON & FORRSTER
FIRMING, INC.
STREET: 755 PINE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
REGISTRATION NUMBER: 27340-20021.00
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221.017B
FILING DATE: 23-DEC-1998

CLASSIFICATION:
PRIOR APPLICATION DATA: P01182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA: P01182
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: P01546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: P02911
FILING DATE: 10-DEC-1998
PRIOR APPLICATION DATA: P02911
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32.430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-8115600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 994:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
STRANDEDNESS: double
SOFTWARE: ASCII text
TOPOLOGY: circular
MOLSCULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE/KEY: misc feature
LOCATION: 1...797

US-09-221-017B-994
Query Match 8.3%; Score 15; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CCCTCCAGCCCAAG 115
Db 422 CCCTCCAGCCCAAG 436

RESULT 13 001C-1175
US-09-134-001C-1175
Best Local Similarity 100.0%; Pred. No. 67;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 TGATTTGAATGTTCT 175
Db 272 TGATTTGAATGTTCT 258

```
RESULT 15
US-08-804-439A-12/c
; Sequence 12, Application US/08804439A
; Patent No. 6015565
; GENERAL INFORMATION:
; APPLICANT: Bose, Timothy M.
; APPLICANT: Bose, Marix L.
; APPLICANT: Strand, Kurt
; TITLE OF INVENTION: GLYCOPROTEIN B OF THE RHV/KSHV
; TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Ste 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/804,439A
; FILING DATE: February 21, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09176/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 785-0070
; TELEFAX: (619) 678-5039
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 2608 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-804-439A-12
;
; Query Match 8.3%; Score 15; DB 3; Length 2608;
; Best Local Similarity 100.0%; Pred.No. 67;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 163 ATTGGAAATGTTCTCT 177
; Db 768 ATTGGAAATGTTCTCT 754
;
; RESULT 16
US-08-720-229-12/c
; Sequence 12, Application US/08720229
; Patent No. 6022412
; GENERAL INFORMATION:
; APPLICANT: Bose, Timothy M.
; APPLICANT: Bose, Marix L.
; APPLICANT: Strand, Kurt
; TITLE OF INVENTION: GLYCOPROTEIN B OF THE RHV/KSHV
; TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,955A
; FILING DATE: October 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025,111
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 09176/0040186
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3258 base pairs
; TYPE: nucleic acid
```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM SOURCE:
; INDIVIDUAL ISOLATE: M2P4
US-08-729-955A-2

Query Match      8.3%; Score 15; DB 2; Length 3258;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 ATGATTGGAAATGTTCT 174
DB 2232 ATGATTGGAAATGTTCT 2246

RESULT 19
US-08-729-214-7
Sequence 7, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
REFERENCE/DOCKET NUMBER: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
PRIORITY INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-7

Query Match      8.3%; Score 15; DB 3; Length 3357;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 CTCACGACCAAGTT 117
DB 2815 CTCACGACCAAGTT 2829

US-08-961-527-143/c
Sequence 143, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 6,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-143

Query Match      8.3%; Score 15; DB 4; Length 4965;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 TGATTGGAAATGTTCT 175
DB 4533 TGATTGGAAATGTTCT 4519

RESULT 20
US-08-961-527-137
Sequence 137, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
```

```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
FAX: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 13440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-137

Query Match      8.3%; Score 15; DB 4; Length 12666;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15c GGTGATGATTCGAAT 170
DB      10747 GGTGATGATTCGAAT 10761

RESULT 21
US-08-961-527-128/c
Sequence 128, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 331
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
PRIORITY NUMBER: US/08/961,527
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
FAX: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 13440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-128

Query Match      8.3%; Score 15; DB 4; Length 13440;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 ACTTATCCGAATTC 15
DB      8919 ACTTATCCGAATTC 8905

RESULT 22
US-08-458-434A-6/c
Sequence 6, Application US/08458434A
Patent No. 5955360
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Stephen E.
APPLICANT: Mungy M.D., Gregory R.
APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
TITLE OF INVENTION: OSTROGENIC AGENTS
SEQUENCE CHARACTERISTICS:
LENGTH: 15144 base pairs
CORRESPONDENCE ADDRESS:
ADDRESSEE: James C. Weesman, Esq.
STREET: 401 B. Street, Suite 1700
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,434A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weesman, James C.
REGISTRATION NUMBER: 30,507
REFERENCE/DOCKET NUMBER: P00060U80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-3604
TELEFAX: 619-236-1048
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-458-434A-6

Query Match      8.3%; Score 15; DB 3; Length 15144;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 GACGCTTCGGAAGG 45
DB      4226 GACGCTTCGGAAGG 4212

RESULT 23
US-08-735-609-4
Sequence 4, Application US/08735609
Patent No. 5955360
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Khatami, Amir
APPLICANT: Kumar Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP

```

```
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; COUNTRY: United States of America
; ZIP: 94104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/08/735,609
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: /desc = "DNA"
;
; US-08-735-609-4
;
; Query Match
; Best Local Similarity 100.0%, Pred. No. 70, Length 34303;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GAGCGTGGAGACGT 35
; DB 8439 GAGCGTGGAGACGT 8453
;
; RESULT 24
; US-09-315-372-4
; Sequence 4, Application US/08735609
; Patent No. 5094132
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/08/735,609
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: /desc = "DNA"
;
; US-08-735-609-4
;
; Query Match
; Best Local Similarity 100.0%, Pred. No. 70, Length 34303;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GAGCGTGGAGACGT 35
; DB 8439 GAGCGTGGAGACGT 8453
;
; RESULT 25
; US-09-315-372-4
; Sequence 4, Application US/0915372
; Patent No. 6057158
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Analfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA: US/09/315,372
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/09/315,372
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: /desc = "DNA"
;
; US-09-315-372-4
;
; Query Match
; Best Local Similarity 100.0%, Pred. No. 70, Length 34303;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GAGCGTGGAGACGT 35
; DB 8439 GAGCGTGGAGACGT 8453
;
; RESULT 26
; US-09-315-372-4
; Sequence 4, Application US/08735609
; Patent No. 5094132
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/08/735,609
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
```

```
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; COUNTRY: United States of America
; ZIP: 94104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/08/735,609
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: /desc = "DNA"
;
; US-08-735-609-4
;
; Query Match
; Best Local Similarity 100.0%, Pred. No. 70, Length 34303;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GAGCGTGGAGACGT 35
; DB 8439 GAGCGTGGAGACGT 8453
;
; RESULT 25
; US-09-315-372-4
; Sequence 4, Application US/0915372
; Patent No. 6057158
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Analfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA: US/09/315,372
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/09/315,372
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: /desc = "DNA"
;
; US-09-315-372-4
;
; Query Match
; Best Local Similarity 100.0%, Pred. No. 70, Length 34303;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GAGCGTGGAGACGT 35
; DB 8439 GAGCGTGGAGACGT 8453
;
; RESULT 26
; US-09-315-372-4
; Sequence 4, Application US/08735609
; Patent No. 5094132
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: US/08/735,609
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
```



```

; FILING DATE: 02-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE: 23-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: INOUE, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UN-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3430 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-562-915-4

Query Match      8.3%  Score 15; DB 4; Length 34303;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 GAGCTGGAGACGCT 35
DB      8439 GAGCTGGAGACGCT 8453

RESULT 29
US-08-374-483-6
; Sequence 6, Application US/08374483
; Patent No. 5880102
; GENERAL INFORMATION:
; APPLICANT: GEORGE, SAMUEL E.
; APPLICANT: BLAZING, MICHAEL A.
; TITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 4100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US/08/374,483
; FILING DATE: 17-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 2,9579-83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3430 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-374-483-6

; FILING DATE: 02-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE: 23-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: INOUE, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UN-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3430 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-562-915-4

Query Match      8.3%  Score 15; DB 2; Length 34382;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 GAGCTGGAGACGCT 35
DB      7859 GAGCTGGAGACGCT 7873

RESULT 30
US-08-973-334-3
; Sequence 3, Application US/08973334
; Patent No. 5880102
; GENERAL INFORMATION:
; APPLICANT: WILSON, JAMES M.
; APPLICANT: FISHER, KRISHNA J.
; APPLICANT: GAO, GUANG-PING
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; TITLE OF INVENTION: Associated Virus, Cell Lines, and
; TITLE OF INVENTION: Methods of Production and Use
; TITLE OF INVENTION: Therapies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 6261551ristown Road
; CITY: Spring House
; STATE: PA, USA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release 1.0 Version 1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08/973,334
; APPLICATION NUMBER: US/08/973,334
; FILING DATE: 08/973,334
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,014
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA: US 08/549,489
; APPLICATION NUMBER: US 08/549,489
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary B.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GRVFN012CIPUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-9181
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
US-08-973-334-3

Query Match      8.3%  Score 15; DB 4; Length 35408;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 GAGCTGGAGACGCT 35
DB      8264 GAGCTGGAGACGCT 8278

RESULT 31
US-09-563-869A-3
; Sequence 3, Application US/09563869A

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; Patent No. 6270896
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; INVENTOR: Gao, Guang-Ping
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; Associated Virus, Cell Lines, and
; Methods of Production and Use
; thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 62709961stTown Road
; CITY: Spring House
; STATE: PA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0 Version 1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/563,869A
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/973,334
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/549,489
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: GNVFN012CIPUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-5206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-563-869A-3

Query Match 8.3%, Score 15; DB 4; Length 35408;
Best Local Similarity 100.0%, Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GACGCTGGAGACGT 35
Db 8264 GACGCTGGAGACGT 8278

RESULT 32
US-08-549-489-3
; Sequence 3, Application US/08549489
; Patent No. 6281010
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; INVENTOR: Gao, Guang-Ping
; TITLE OF INVENTION: Adenovirus Gene Therapy Vehicle
; and Cell Line
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 62810101stTown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA

; Patent No. 6270896
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; INVENTOR: Gao, Guang-Ping
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; Associated Virus, Cell Lines, and
; Methods of Production and Use
; thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 62709961stTown Road
; CITY: Spring House
; STATE: PA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0 Version 1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/563,869A
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/973,334
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/549,489
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: GNVFN012CIPUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-5206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-563-869A-3

Query Match 8.3%, Score 15; DB 4; Length 35408;
Best Local Similarity 100.0%, Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GACGCTGGAGACGT 35
Db 8264 GACGCTGGAGACGT 8278

RESULT 33
US-08-735-609-1
; Sequence 1, Application US/08735609
; Patent No. 6281010
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE: 08-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338

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/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35935 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ US-08-735-609-1

Query Match 8.3%; Score 15; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCGCTGGAGACCT 35
DB 6936 GAGCGCTGGAGACCT 6950

RESULT 34
US-08-735-609-1
Sequence 1; Application US/08735609
Patent No. 5994132

/ GENERAL INFORMATION:
/ APPLICANT: Chamberlain, Jeffrey S.
/ Analfitano, Michael A.

/ Kumar-Singh, Rajendra
/ Harteigan-O'Connor, Dennis J.
/ TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS

/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Medlen & Carroll, LLP

/ STREET: 220 Montgomery Street, Suite 2200
/ CITY: San Francisco
/ STATE: California

/ COUNTRY: United States Of America
/ ZIP: 94104

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION NUMBER: US/08/735,609
/ FILING DATE: 23-Oct-1996

/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ingolla, Diane E.

/ REGISTRATION NUMBER: 40,027
/ REFERENCE/DOCKET NUMBER: UM-02484

/ TELECOMMUNICATIONS INFORMATION:
/ TELEPHONE: (415) 705-8410
/ TELEFAX: (415) 397-8338

/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35935 base pairs

/ TYPE: nucleic acid
/ STRANDEDNESS: double

/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"

/ US-08-735-609-1

QY 21 GAGCGCTGGAGACCT 35
DB 6936 GAGCGCTGGAGACCT 6950

Query Match 8.3%; Score 15; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35

US-08-379-452-43

/ Sequence 1; Application US/08379452
/ Patent No. 5994132

/ GENERAL INFORMATION:
/ APPLICANT: Ingler, Jean-Luc

/ APPLICANT: MEHTALI, Majid
/ APPLICANT: PAVIRANI, Andrea

/ TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
/ COMPLEMENTATION LINES

/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

/ STREET: 1737 King Street, Suite 500
/ CITY: Alexandria

/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22314-2756

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,452
/ FILING DATE: 26-JAN-1995

/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/FR94/00624

/ FILING DATE: 27-MAY-1994
/ PRIOR APPLICATION NUMBER: FR 93 06482

/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ingolla, Diane E.

/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 029395-002

/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35935 base pairs

/ TYPE: nucleic acid
/ STRANDEDNESS: single

/ MOLECULE TYPE: DNA (genomic)
/ US-08-379-452-43

QY 21 GAGCGCTGGAGACCT 35
DB 6936 GAGCGCTGGAGACCT 6950

RESULT 36

US-09-315-372-1

/ Sequence 1; Application US/09315372
/ Patent No. 6097158

/ GENERAL INFORMATION:
/ APPLICANT: Chamberlain, Jeffrey S.

/ APPLICANT: Analfitano, Michael A.
/ APPLICANT: Kumar-Singh, Rajendra

/ TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
/ NUMBER OF SEQUENCES: 15

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Medlen & Carroll, LLP

/ STREET: 220 Montgomery Street, Suite 2200
/ CITY: San Francisco
/ STATE: California

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; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
; FILING DATE: US/09/315,372
; APPLICATION NUMBER: US/09/244,752
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/735,609
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3595 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-315-372-1
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; Query Match 8.3%; Score 15; DB 3; Length 35935;
; Best Local Similarity 100.0%; Freq. No. 70;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 21 GACGCTGGAGAGCGT 35
; DB 6936 GACGCTGGAGAGCGT 6950
;
; RESULT 38
; US-09-244-752-1
; Sequence 1, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Michael A.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
; FILING DATE: US/09/245,497
; APPLICATION NUMBER: US/09/245,497
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,609
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3595 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-244-752-1
;
; Query Match 8.3%; Score 15; DB 3; Length 35935;
; Best Local Similarity 100.0%; Freq. No. 70;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GACGCTGGAGAGCGT 35
; DB 6936 GACGCTGGAGAGCGT 6950
;
; RESULT 37
; US-09-244-752-1
; Sequence 1, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Michael A.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
; FILING DATE: US/09/244,752
; APPLICATION NUMBER: US/09/244,752
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,609
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
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; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
; FILING DATE: US/09/315,372
; APPLICATION NUMBER: US/09/244,752
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/735,609
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3595 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-244-752-1
;
; Query Match 8.3%; Score 15; DB 3; Length 35935;
; Best Local Similarity 100.0%; Freq. No. 70;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 21 GACGCTGGAGAGCGT 35
; DB 6936 GACGCTGGAGAGCGT 6950
;
; RESULT 38
; US-09-245-497-1
; Sequence 1, Application US/09245497
; Patent No. 6083750
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Michael A.
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
; FILING DATE: US/09/245,497
; APPLICATION NUMBER: US/09/245,497
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,609
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3595 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-245-497-1
;
; Query Match 8.3%; Score 15; DB 3; Length 35935;
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Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 39
US-09-409-670-43
; Sequence 43, Application US/09409670
; Patent No. 6113028
; GENERAL INFORMATION:
; APPLICANT: Jean-Luc
; APPLICANT: MERTALLI, Majid
; APPLICANT: PAVRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; STREET: 1737 Kings Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MOLECULE TYPE: copy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,670
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Padio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-409-670-43

Query Match 8.3%; Score 15; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 40
US-09-562-919-1
; Sequence 1, Application US/09562919
; Patent No. 6451596
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Anaiftano, Andrea
; APPLICANT: Hauser, Michael A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

Query Match 8.3%; Score 15; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 41
US-09-562-919-1
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Preiner, N
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

Query Match 8.3%; Score 15; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 42
US-09-562-919-1
; Sequence 1, Application US/09562919
; Patent No. 6451596
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Anaiftano, Andrea
; APPLICANT: Hauser, Michael A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 39
US-09-409-670-43
; Sequence 43, Application US/09409670
; Patent No. 6113028
; GENERAL INFORMATION:
; APPLICANT: Jean-Luc
; APPLICANT: MERTALLI, Majid
; APPLICANT: PAVRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; STREET: 1737 Kings Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MOLECULE TYPE: copy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/562,919
; FILING DATE: 02-MAY-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE: 23-Oct-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UN-02484
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-562-919-1

Query Match 8.3%; Score 15; DB 4; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 41
US-09-562-919-1
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Preiner, N
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

Query Match 8.3%; Score 15; DB 4; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 41
US-09-562-919-1
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Preiner, N
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

Query Match 8.3%; Score 15; DB 4; Length 35935;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GAGCTGGAGACGT 35
DB 6936 GAGCTGGAGACGT 6950

RESULT 42
US-09-562-919-1
; Sequence 1, Application US/09562919
; Patent No. 6451596
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Anaiftano, Andrea
; APPLICANT: Hauser, Michael A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: TREATING CHRONIC-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7

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; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, o r t
US-09-268-992-7

Query Match      8.3%; Score 15; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 70; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 161 TGAATGGAATGTCT 175
Db 71962 TGAATGGAATGTCT 71976

RESULT 42
US-09-657-474-7
; Sequence 7; Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; LOCATION: Fremont, N
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; AND TREATING CHROMOSOME-19p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ IDS NOS: 84
; SEQ ID NO 7 FastSeq for Windows Version 3.0
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, o r t
US-09-657-474-7

Query Match      8.3%; Score 15; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 70; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 161 TGAATGGAATGTCT 175
Db 71962 TGAATGGAATGTCT 71976

RESULT 43
US-08-584-040-7504/c
; Sequence 7504; Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
; CONDITIONS RELATED TO LEVELS
; OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:

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; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT FILING DATE: 1998-03-16
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McSwiggen, James J.
; REGISTRATION NUMBER: 137
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 7504:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72604 bp
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7504

Query Match      7.7%; Score 14; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

Qy 34 GTCTTCGAAGGAT 47
Db 17 GTCTTCGAAGGAT 4

RESULT 44
US-08-584-040-7505/c
; Sequence 7505; Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
; CONDITIONS RELATED TO LEVELS
; OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; CURRENT APPLICATION DATA: Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weidburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 7505:
; LENGTH: 34 base pairs
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7505

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 34 GTCTTCGGAAGCAT 47
Db 16 GTCTTCGGAAGCAT 3

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RESULT 45
US-08-062-368-12
; Sequence 12, Application US/08062368
; Patent No. 5491086
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
; TITLE OF INVENTION: Polymersase Enzyme From Pyrodictum Species
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingdland Street
; CITY: Nutley, New Jersey
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/062,368
; FILING DATE: 19930514
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-062-368-12
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Length 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 87 AGCTGACGACGAGG 100
Db 4 AGCTGACGACGAGG 17

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Search completed: June 9, 2003, 12:46:53
Job time : 98 secs

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84	16	8	8	622	21	AAH20297	Human colon cancer	C 157	15	8	3	231	21	AAAC1901	Cat flea hindgut a
85	16	8	8	761	23	ABL19125	Drosophila melanog	C 158	15	8	3	246	21	AAQ31969	Human breast cell
86	16	8	8	795	22	AAK82908	Human immune/haema	C 159	15	8	3	271	22	ABR49762	Human foetal liver
87	16	8	8	1077	22	AAH32014	Human oifactory re	C 160	15	8	3	271	22	ABR43742	Probe #1208 for g
88	16	8	8	1074	22	AAH32005	Human oifactory re	C 161	15	8	3	271	22	ABR43742	Human brain expres
89	16	8	8	1100	21	AAH75819	Human ORFX ORF1374	C 162	15	8	3	271	22	AAK160592	Human brain expres
90	16	8	8	1412	22	AAH189310	Human polynucleoti	C 163	15	8	3	271	22	AAK122600	Probe #1253 for g
91	16	8	8	1528	22	AAH189310	Human polynucleoti	C 164	15	8	3	271	22	AAK122600	Probe #1253 for g
92	16	8	8	1528	22	AAH169716	Human polynucleoti	C 165	15	8	3	271	22	AAI08276	Probe #16578 used t
93	16	8	8	1559	22	AAH158929	Human polynucleoti	C 166	15	8	3	271	22	AAI08276	Probe #8267 used t
94	16	8	8	1593	22	AAH291442	Polynucleotide seq	C 167	15	8	3	271	22	AAH158857	Human genome-deriv
95	16	8	8	1665	22	AAH199104	Human excretory re	C 168	15	8	3	273	21	AAAS1791	N. meningitidis pa
96	16	8	8	1665	22	AAH163454	Human kidney relat	C 169	15	8	3	273	21	AAAS1791	Human breast cell
97	16	8	8	1750	21	AAH47992	Arabidopsis thalia	C 170	15	8	3	274	22	ABR48663	Human foetal liver
98	16	8	8	1902	22	AAH58105	Human GTP-binding	C 171	15	8	3	274	22	ABR48663	Human foetal liver
99	16	8	8	2117	22	AAH58105	Human GTP-binding	C 172	15	8	3	274	22	ABR48663	Human foetal liver
100	16	8	8	2117	21	AAH31093	Arabidopsis thalia	C 173	15	8	3	274	22	ABR43718	Probe #12184 for g
101	16	8	8	2228	22	AAH16361	Human cDNA sequenc	C 174	15	8	3	274	22	ABR43718	Human brain expres
102	16	8	8	2244	24	ABL65864	Lung cancer relate	C 175	15	8	3	274	22	AAK15082	Human brain expres
103	16	8	8	2244	24	ABL66528	Lung cancer relate	C 176	15	8	3	274	22	AAK15082	Human brain expres
104	16	8	8	2278	23	ABL18693	Drosophila melanog	C 177	15	8	3	274	22	AAK10810	Human bone marrow
105	16	8	8	2326	4	AAH30174	Sequence of the Li	C 178	15	8	3	274	22	AAK10810	Human bone marrow
106	16	8	8	3216	15	AAQ56832	Small round virus	C 179	15	8	3	274	22	AAI215580	Probe #11513 for g
107	16	8	8	3812	21	AAH19324	Drosophila melanog	C 180	15	8	3	274	22	AAH15555	Probe #11555 used
108	16	8	8	3812	21	AAH19324	Drosophila melanog	C 181	15	8	3	274	22	AAH15555	Probe #11555 used
109	16	8	8	3880	21	AAH78021	Human cancer assoc	C 182	15	8	3	274	22	AAI070524	Probe #15742 used
110	16	8	8	3890	21	AAH293781	Human desmin prom	C 183	15	8	3	274	22	AAI070524	Probe #7265 used t
111	16	8	8	3893	21	AAH38444	Human desmin gene	C 184	15	8	3	274	22	AAI07459	Probe #7450 used t
112	16	8	8	3900	24	AAK63943	cDNA encoding huma	C 185	15	8	3	274	22	ABR41764	Human genome-deriv
113	16	8	8	3970	20	AAH200390	Borrelia burgdorferi	C 186	15	8	3	295	24	ABR41764	Human genome-deriv
114	16	8	8	3315	22	AAH30486	Barley stripe RNA	C 187	15	8	3	321	22	AAH30486	Human genome-deriv
115	16	8	8	4294	22	AAK66072	Human immune/haema	C 188	15	8	3	321	22	ABR43251	Breast cancer relat
116	16	8	8	4294	22	AAK66072	Human immune/haema	C 189	15	8	3	369	22	AAH38319	Novel human diagn
117	16	8	8	5004	23	ABL16592	Drosophila melanog	C 190	15	8	3	378	24	ABR46466	Human benign pro
118	16	8	8	5807	24	ABL33155	Human immune syste	C 191	15	8	3	389	24	ABR46466	Human cancer relat
119	16	8	8	5862	24	ABL33286	Human immune syste	C 192	15	8	3	402	24	ABR31064	Human cancer relat
120	16	8	8	5993	22	AAK53105	Human polynucleoti	C 193	15	8	3	402	24	ABR31064	M. capsulatus gene
121	16	8	8	5993	22	AAK53106	Human polynucleoti	C 194	15	8	3	402	24	ABR31064	Human prostate exp
122	16	8	8	6047	24	ABL65188	Lung cancer relate	C 195	15	8	3	412	24	ABR7032	Human prostate exp
123	16	8	8	6047	24	ABL65188	Lung cancer relate	C 196	15	8	3	412	24	ABR7032	Human prostate exp
124	16	8	8	6567	22	AAK52321	Human polynucleoti	C 197	15	8	3	415	24	ABR7032	Human prostate exp
125	16	8	8	7170	23	ABL11029	Drosophila melanog	C 198	15	8	3	420	19	AAH10365	Human ORFX polynuc
126	16	8	8	7722	15	AAQ12023	Norwalk virus geno	C 199	15	8	3	425	20	AAH13111	FRAP homolog. Cry
127	16	8	8	7753	15	AAQ56826	Norwalk virus geno	C 200	15	8	3	429	24	ABR26114	Human secreted pro
128	16	8	8	8283	23	ABL10886	Drosophila melanog	C 201	15	8	3	433	24	ABR26114	Human ORFX polynuc
129	16	8	8	9826	23	ABL11028	Drosophila melanog	C 202	15	8	3	433	24	ABR26114	Human prostate exp
130	16	8	8	11890	24	ABL69703	Prostate cancer	C 203	15	8	3	455	22	AAH07207	Human reproductive
131	16	8	8	11890	24	ABL69703	Prostate cancer	C 204	15	8	3	455	22	AAH07207	Human reproductive
132	16	8	8	14796	19	AAH27941	Survivin gene. Ho	C 205	15	8	3	455	22	ABR23837	Human foetal liver
133	16	8	8	14796	22	AAH21523	DNA encoding human	C 206	15	8	3	455	22	AAK02360	Human brain expres
134	16	8	8	14796	22	AAH7531	Human Her-3 genom	C 207	15	8	3	455	22	AAK27802	Human bone marrow
135	16	8	8	14796	24	ABR56924	Gene #3422 used to	C 208	15	8	3	455	22	AAI12387	Probe #2320 for ge
136	16	8	8	14796	24	ABR56924	Gene #3422 used to	C 209	15	8	3	455	22	AAI12387	Probe #2320 for ge
137	16	8	8	14796	24	ABR56924	Gene #3422 used to	C 210	15	8	3	455	22	AAI12387	Probe #2320 for ge
138	16	8	8	14796	24	ABR56924	Gene #3422 used to	C 211	15	8	3	455	22	AAI12387	Probe #2320 for ge
139	16	8	8	14796	24	ABR56924	Gene #3422 used to	C 212	15	8	3	455	22	AAI12387	Probe #2320 for ge
140	16	8	8	32192	22	AAK69452	Human digestive sy	C 213	15	8	3	472	22	ABR44615	Human breast cell
141	16	8	8	53585	20	AAK02051	Borrelia burgdorferi	C 214	15	8	3	472	22	ABR44615	Human foetal liver
142	16	8	8	144460	21	AAH293815	Olfactory receptor	C 215	15	8	3	472	22	ABR44615	Probe #3287 for ge
143	16	8	8	267156	24	ABL68560	Kidney cancer rela	C 216	15	8	3	472	22	AAK03332	Human brain expres
144	16	8	8	640681	24	AAH292787	Buchnera sp. genom	C 217	15	8	3	472	22	AAK03332	Human bone marrow
145	16	8	8	23655589	24	AAH305021	Genomic sequenc o	C 218	15	8	3	472	22	AAK03332	Probe #3302 for ge
146	16	8	8	23655589	24	AAH305021	Genomic sequenc o	C 219	15	8	3	472	22	AAK03332	Probe #3302 for ge
147	15	8	3	2394428	21	AAH202455	PCR primer used	C 220	15	8	3	472	22	AAI01263	Probe #13254 used t
148	15	8	3	21	22	AAZ02465	Human foetal liver	C 221	15	8	3	472	22	ABR033308	Human genome-deriv
149	15	8	3	81	22	ABR42048	Human foetal liver	C 222	15	8	3	472	22	ABR42048	Human foetal liver
150	15	8	3	81	22	ABR42048	Human foetal liver	C 223	15	8	3	472	22	ABR42048	Human foetal liver
151	15	8	3	81	22	AAK46614	Human brain expres	C 224	15	8	3	475	22	AAK025566	Human brain expres
152	15	8	3	81	22	AAK46614	Human brain expres	C 225	15	8	3	475	22	AAK025566	Human brain expres
153	15	8	3	81	22	AAK46614	Human brain expres	C 226	15	8	3	475	22	AAK025566	Probe #2319 used g
154	15	8	3	81	22	AAK46614	Human brain expres	C 227	15	8	3	475	22	AAK025566	Probe #2319 used g
155	15	8	3	158	24	AAH169095	Activated T-cell d	C 228	15	8	3	475	22	AAH169095	Probe #2482 used t

C 375	15	8.3	4927	24	Listeria monocytog
C 376	15	8.3	4965	21	Streptococcus pneu
C 377	15	8.3	5248	21	Drosophila melanog
C 378	15	8.3	5248	21	Chemically treated
C 379	15	8.3	5261	24	Human gene regulat
C 380	15	8.3	5261	24	Human immune syste
C 381	15	8.3	5559	24	Drosophila melanog
C 382	15	8.3	5736	23	DNA encoding novel
C 383	15	8.3	5736	23	Chemically pretrea
C 384	15	8.3	5774	24	DNA transcrip
C 385	15	8.3	5774	24	DNA encoding novel
C 386	15	8.3	5799	23	Chemically pretrea
C 387	15	8.3	6022	22	Chemically pretrea
C 388	15	8.3	6022	22	Human suppressor
C 389	15	8.3	6022	22	Human transcrip
C 390	15	8.3	6022	22	DNA transcrip
C 391	15	8.3	6103	24	Human immune syste
C 392	15	8.3	6103	24	Signal transductio
C 393	15	8.3	6161	24	Drosophila melanog
C 394	15	8.3	6224	23	Drosophila melanog
C 395	15	8.3	6319	21	Human ORF ORF274
C 396	15	8.3	6319	21	Human ORF ORF274
C 397	15	8.3	6881	24	Human immun
C 398	15	8.3	6881	24	DNA transcrip
C 399	15	8.3	6883	23	Drosophila melanog
C 400	15	8.3	7231	21	Nucleotide sequenc
C 401	15	8.3	7231	21	Nucleotide sequenc
C 402	15	8.3	7406	24	Human chemically m
C 403	15	8.3	7414	24	Human chemically m
C 404	15	8.3	7414	24	Human chemically m
C 405	15	8.3	7601	22	Human musculoskele
C 406	15	8.3	7601	22	Human musculoskele
C 407	15	8.3	7960	24	Nucleotide sequenc
C 408	15	8.3	7960	24	Nucleotide sequenc
C 409	15	8.3	7989	24	Nucleotide sequenc
C 410	15	8.3	7989	24	Nucleotide sequenc
C 411	15	8.3	8381	21	Human immune/haema
C 412	15	8.3	8381	21	Nucleotide sequenc
C 413	15	8.3	8383	24	Nucleotide sequenc
C 414	15	8.3	8484	21	Nucleotide sequenc
C 415	15	8.3	9431	23	Drosophila melanog
C 416	15	8.3	9721	23	Drosophila melanog
C 417	15	8.3	9951	23	Drosophila melanog
C 418	15	8.3	10312	22	Human immune/haema
C 419	15	8.3	10312	22	Nucleotide sequenc
C 420	15	8.3	10668	23	Drosophila melanog
C 421	15	8.3	11960	22	Human reproductiv
C 422	15	8.3	11960	22	Human testicular
C 423	15	8.3	11991	22	Human musculoskele
C 424	15	8.3	11991	22	Human reproductiv
C 425	15	8.3	12027	23	DNA encoding novel
C 426	15	8.3	12027	23	Drosophila melanog
C 427	15	8.3	12593	23	Streptococcus pneu
C 428	15	8.3	12593	23	Streptococcus pneu
C 429	15	8.3	12593	23	Streptococcus pneu
C 430	15	8.3	12666	19	Human genomic DNA
C 431	15	8.3	13133	23	DNA encoding enzym
C 432	15	8.3	13133	23	Human suppressor
C 433	15	8.3	13137	22	Human gene regulat
C 434	15	8.3	13137	22	Human immune/haema
C 435	15	8.3	13440	19	Streptococcus pneu
C 436	15	8.3	14176	22	Human genomic DNA
C 437	15	8.3	14245	21	Nucleotide sequenc
C 438	15	8.3	14245	21	Mouse bone morphog
C 439	15	8.3	15273	18	Human immune/haema
C 440	15	8.3	16273	22	Human immune/haema
C 441	15	8.3	16273	22	Human immune/haema
C 442	15	8.3	16273	22	Human immune/haema
C 443	15	8.3	17727	23	DNA encoding novel
C 444	15	8.3	19131	22	Tumour suppressor
C 445	15	8.3	19861	23	DNA encoding novel
C 446	15	8.3	21129	22	Human cardiavascu
C 447	15	8.3	21747	23	Drosophila melanog
C 448	15	8.3	21747	23	Drosophila melanog
C 449	15	8.3	21747	23	Drosophila melanog
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C 590	15	8.3	21747	23	Drosophila melanog
C 591	15	8.3	21747	23	Drosophila melanog
C 592	15	8.3	21747	23	Drosophila melanog
C 593	15	8.3	21747	23	Drosophila melanog
C 594	15	8.3	21747	23	Drosoph

c 667	14	7.7	401	19	AAV40728	C. felis esterase,	740	14	7.7	458	22	AA05585	Human reproductive
c 668	14	7.7	401	22	ADAD2163	Ctenocephalides fe	c 741	14	7.7	458	22	AAE68129	Human lung tumour
c 669	14	7.7	405	23	ABV35055	Human prostate exp	c 742	14	7.7	459	24	ABK30040	cDNA encoding clon
c 670	14	7.7	405	23	ABV37801	Human prostate exp	c 743	14	7.7	463	24	ABQ58465	Human colon cancer
c 671	14	7.7	407	23	ABV37057	Human prostate exp	c 744	14	7.7	463	24	ABQ58465	Human colon cancer
c 672	14	7.7	408	23	ABV44789	Human prostate exp	c 745	14	7.7	465	24	ABV36439	Human colon tumour
c 673	14	7.7	411	22	ABA44789	Human prostate exp	c 746	14	7.7	465	24	ABV46977	Human prostate exp
c 674	14	7.7	411	22	ABA45244	Human foetal liver	c 747	14	7.7	470	22	AAI06977	Human breast cancer
c 675	14	7.7	411	22	ABA42491	Probe #3457 for ge	c 748	14	7.7	470	22	AAQ36433	Human cardiovascular
c 676	14	7.7	411	22	AKO31502	Human brain expres	c 749	14	7.7	471	22	AAE74729	Human foetal liver
c 677	14	7.7	411	22	AAI13542	Probe #3475 for ge	c 750	14	7.7	471	22	ABQ39440	Human foetal liver
c 678	14	7.7	411	22	AAI34904	Probe #3590 used t	c 751	14	7.7	471	22	AAI13528	Probe #17906 for g
c 679	14	7.7	411	22	AAI03431	Probe #3422 used t	c 752	14	7.7	471	22	AAI13528	Probe #17906 for g
c 680	14	7.7	411	22	AAI03431	Probe #3422 used t	c 753	14	7.7	471	22	AAI13528	Probe #17906 for g
c 681	14	7.7	412	22	AAK96420	Human neuregulin g	c 754	14	7.7	471	22	AAI58249	Probe #23935 used
c 682	14	7.7	412	22	AAK96420	Human neuregulin g	c 755	14	7.7	471	22	AAI04950	Probe #4981 used t
c 683	14	7.7	413	22	ABA5881	Human breast cell	c 756	14	7.7	471	22	AAE80459	Nucleotide sequenc
c 684	14	7.7	413	22	ABA5881	Human breast cell	c 757	14	7.7	471	22	ABE28274	Human genome-deriv
c 685	14	7.7	413	22	ABA56403	Human foetal liver	c 758	14	7.7	473	22	AAO09511	Human breast cancer
c 686	14	7.7	413	22	AKA4573	Probe #4499 for ge	c 759	14	7.7	474	22	AAK04984	Human brain expres
c 687	14	7.7	413	22	AKA4573	Human brain expres	c 760	14	7.7	476	22	ABE82766	Human foetal liver
c 688	14	7.7	413	22	AAI03076	Probe #4603 for ge	c 761	14	7.7	476	22	ABE82766	Human foetal liver
c 689	14	7.7	413	22	AAI16039	Probe #4725 used t	c 762	14	7.7	478	22	AAK06374	Human brain expres
c 690	14	7.7	413	22	AAI04481	Probe #4472 used t	c 763	14	7.7	478	22	AAK32042	Human bone marrow
c 691	14	7.7	413	22	ABE04652	Human genome-deriv	c 764	14	7.7	478	24	ABE06809	Human genome-deriv
c 692	14	7.7	415	22	ABR45430	Human breast cell	c 765	14	7.7	480	21	AAQ35313	Myrtaceae microsat
c 693	14	7.7	415	22	ABR45430	Human foetal liver	c 766	14	7.7	480	21	AAQ35313	DNA encoding novel
c 694	14	7.7	415	22	ABR45430	Probe #4061 for ge	c 767	14	7.7	483	22	AAE27724	DNA encoding nove
c 695	14	7.7	415	22	ABR45430	Human bone marrow	c 768	14	7.7	483	22	AAE27724	Human prostate exp
c 696	14	7.7	415	22	AAI29623	Human bone marrow	c 769	14	7.7	483	24	ABV31850	Human prostate exp
c 697	14	7.7	415	22	AAI14202	Probe #4135 for ge	c 770	14	7.7	483	24	AAE61706	Lung small cell ca
c 698	14	7.7	415	22	AAI35583	Probe #4269 used t	c 771	14	7.7	483	24	AAE61853	Lung small cell ca
c 699	14	7.7	415	22	AAI04039	Probe #4030 used t	c 772	14	7.7	484	21	AAE48122	Zea mays DNA fragm
c 700	14	7.7	415	22	ABE04179	Human genome-deriv	c 773	14	7.7	487	23	ABV13119	Human prostate exp
c 701	14	7.7	416	22	AAI93350	Human polynucleoti	c 774	14	7.7	498	20	AAE37489	Human prostate exp
c 702	14	7.7	424	24	ABV49874	Human prostate exp	c 775	14	7.7	498	20	AAE37489	Rat U1 gene trap d
c 703	14	7.7	424	24	ABV49874	Human prostate exp	c 776	14	7.7	501	22	AAE37489	C. glutamicum SRT
c 704	14	7.7	429	23	ABV17182	Human prostate exp	c 777	14	7.7	501	22	AAE37489	Human transcripti
c 705	14	7.7	433	23	ABV58447	cDNA #1123 encodin	c 778	14	7.7	507	13	AAQ12658	LEHMI 10 cDNA. Ly
c 706	14	7.7	434	24	ABK54663	Human colon cancer	c 779	14	7.7	507	13	AAQ12658	Human nervous syst
c 707	14	7.7	435	24	AAE79993	Human polynucleoti	c 780	14	7.7	507	22	AAI05096	Human reproductive
c 708	14	7.7	444	24	AAE92336	Bovine mammary tis	c 781	14	7.7	507	23	ABV97989	Human testicular a
c 709	14	7.7	444	24	ABV46597	Human colon tumour	c 782	14	7.7	508	22	AAE27729	Human immune/haema
c 710	14	7.7	444	24	ABV46597	Human colon tumour	c 783	14	7.7	516	23	ABV47626	Human testicular a
c 711	14	7.7	448	24	ABK60966	Human cancer relat	c 784	14	7.7	516	23	ABV47626	Human prostate exp
c 712	14	7.7	448	24	ABK64670	Stomach cancer relat	c 785	14	7.7	517	23	AAE66069	DNA encoding novel
c 713	14	7.7	450	22	ABR44797	Human breast cell	c 786	14	7.7	520	16	AAQ02909	Rat beta amyloid f
c 714	14	7.7	450	22	ABR44797	Human foetal liver	c 787	14	7.7	520	16	AAQ02910	Human beta amyloid
c 715	14	7.7	450	22	ABR45252	Human foetal liver	c 788	14	7.7	520	24	ABE58332	Human colon cancer
c 716	14	7.7	450	22	ABR45258	Probe #3463 for ge	c 789	14	7.7	522	22	ABV13395	Human nervous syst
c 717	14	7.7	450	22	ABR45258	Probe #3463 for ge	c 790	14	7.7	522	22	ABV13395	Human nervous syst
c 718	14	7.7	450	22	ABR45258	Probe #3463 for ge	c 791	14	7.7	524	24	AAE37489	Human prostate exp
c 719	14	7.7	450	22	AAK03508	Human brain expres	c 792	14	7.7	524	24	AAE37489	Porcine muscular s
c 720	14	7.7	450	22	AAK03508	Human brain expres	c 793	14	7.7	525	21	AAE379029	Human secreted pro
c 721	14	7.7	450	22	AAK07471	Human bone marrow	c 794	14	7.7	527	24	AAE614259	Human immune/haema
c 722	14	7.7	450	22	AAK32962	Human bone marrow	c 795	14	7.7	527	24	ABK44559	cDNA encoding colo
c 723	14	7.7	450	22	AAI13549	Probe #3482 for ge	c 796	14	7.7	529	22	ABV17175	Human foetal liver
c 724	14	7.7	450	22	AAI13549	Probe #3597 used t	c 797	14	7.7	529	22	ABV17856	Human foetal liver
c 725	14	7.7	450	22	AAI13549	Probe #3597 used t	c 798	14	7.7	529	22	AAE20144	Human brain expres
c 726	14	7.7	450	22	AAI13549	Probe #3597 used t	c 799	14	7.7	529	22	AAE20144	Human brain expres
c 727	14	7.7	450	24	ABE03486	Human genome-deriv	c 800	14	7.7	529	22	AAI25565	Human bone marrow
c 728	14	7.7	450	24	ABE03486	Human genome-deriv	c 801	14	7.7	529	22	AAI25565	Probe #15498 for g
c 729	14	7.7	456	22	ABA43700	Human breast cell	c 802	14	7.7	529	22	AAI52110	Probe #20796 used
c 730	14	7.7	456	22	ABA43700	Human foetal liver	c 803	14	7.7	529	24	ABE20515	Human genome-deriv
c 731	14	7.7	456	22	ABK24391	Probe #2167 for ge	c 804	14	7.7	530	24	ABK24391	Rat sequence diff
c 732	14	7.7	456	22	ABK24391	Human brain expres	c 805	14	7.7	532	22	AAE28827	Drosophila melanog
c 733	14	7.7	456	22	ABK24391	Human brain expres	c 806	14	7.7	532	22	AAE28827	Human colon cancer
c 734	14	7.7	456	22	ABK24391	Human brain expres	c 807	14	7.7	533	24	AAE28827	Human colon cancer
c 735	14	7.7	456	22	AAI13804	Probe #2382 for ge	c 808	14	7.7	534	22	AAE28827	Human testicular a
c 736	14	7.7	456	22	AAI13804	Probe #2490 used t	c 809	14	7.7	536	21	AAE28827	Murine 7-transmemb
c 737	14	7.7	456	22	ABE02360	Probe #2351 used t	c 810	14	7.7	536	21	AAE28827	Human ORFX ORP2C51
c 738	14	7.7	456	24	ABE02360	Human genome-deriv	c 811	14	7.7	542	23	AAE28827	C. glutamicum SRT
c 739	14	7.7	458	21	AAE09542	Ovary cancer relat	c 812	14	7.7	547	22	AAE28827	Human prostate exp
c 740	14	7.7	458	21	AAE09542	Human prostate exp	c 813	14	7.7	547	22	AAE28827	Human prostate exp

C 813	14	7, 7	547	24	ABK30884	cDNA encoding clon	C 886	14	7, 7	637	23	ABW40144	Human prostate exp
C 814	14	7, 7	549	21	AAK32927	Human testicular a	C 887	14	7, 7	638	23	AAK32927	Human prostate exp
C 815	14	7, 7	552	22	ABK60637	Human testicular a	C 888	14	7, 7	639	23	ASB11333	Human prostate exp
C 816	14	7, 7	552	22	AAK28744	Probe #7210 for ge	C 889	14	7, 7	639	22	AAK52698	S epidermidis ope
C 817	14	7, 7	552	22	AAK08919	Human brain expres	C 890	14	7, 7	640	22	AAK52698	Human immune/haema
C 818	14	7, 7	552	22	AAK34809	Human bone marrow	C 891	14	7, 7	645	24	ABQ86213	Lactobacillus rham
C 819	14	7, 7	552	22	AAK440528	Probe #9214 used t	C 892	14	7, 7	649	24	ABQ59974	Human colon cancer
C 820	14	7, 7	552	24	AAK093358	Human genome-deriv	C 893	14	7, 7	650	22	AAK64518	Human immune/haema
C 821	14	7, 7	552	24	AAK093358	Human genome-deriv	C 894	14	7, 7	650	22	AAK64518	Protophilla melanog
C 822	14	7, 7	557	24	ABQ44439	Oligonucleotide fo	C 895	14	7, 7	650	22	AAK64518	Human prostate exp
C 823	14	7, 7	557	24	ABQ44439	Human prostate exp	C 896	14	7, 7	653	24	ABL98903	Human polynucleoti
C 824	14	7, 7	560	23	AAK594336	Human prostate exp	C 897	14	7, 7	653	24	ABL98903	Human secreted pro
C 825	14	7, 7	561	22	AAH77920	Nucleotide sequenc	C 898	14	7, 7	655	21	AAK31368	Human polynucleoti
C 826	14	7, 7	570	22	AAK63981	Human foetal liver	C 899	14	7, 7	655	22	AAK31368	Human polynucleoti
C 827	14	7, 7	570	22	AAK31152	Probe #9618 for ge	C 900	14	7, 7	657	23	ABY16713	Human prostate exp
C 828	14	7, 7	570	22	AAK12478	Human brain expres	C 901	14	7, 7	661	22	AA193354	Human polynucleoti
C 829	14	7, 7	570	22	AAK38188	Human bone marrow	C 902	14	7, 7	661	24	AAQ39384	Human colon cancer
C 830	14	7, 7	570	22	AAK38188	Human bone marrow	C 903	14	7, 7	662	21	AAQ39384	Aspergillus oryzae
C 831	14	7, 7	570	22	AA141419	Probe #12805 for ge	C 904	14	7, 7	668	21	AAQ39384	Human prostate exp
C 832	14	7, 7	570	22	AAK32222	Human genome-deriv	C 905	14	7, 7	674	23	ABV22418	Human prostate exp
C 833	14	7, 7	572	22	AAK18495	Human breast canc	C 906	14	7, 7	674	23	ABV22418	Human prostate exp
C 834	14	7, 7	572	22	AAK51541	Human prostate exp	C 907	14	7, 7	675	24	AAK562171	Porcine muscular s
C 835	14	7, 7	573	22	AAK37952	Human prostate exp	C 908	14	7, 7	677	21	AAK45257	Arabidopsis thalia
C 836	14	7, 7	578	21	AAK78135	cDNA encoding huma	C 909	14	7, 7	677	21	AAK45257	Arabidopsis thalia
C 837	14	7, 7	578	24	AAK39818	Colon tumour relat	C 910	14	7, 7	687	24	ABR490333	Human polynucleoti
C 838	14	7, 7	578	24	AAK39818	Human prostate exp	C 911	14	7, 7	691	24	ABQ57054	Human colon cancer
C 839	14	7, 7	579	22	AAK08923	Human breast canc	C 912	14	7, 7	700	24	AAK56957	Human polynucleoti
C 840	14	7, 7	580	24	AAK61567	Lung small cell ca	C 913	14	7, 7	700	22	AAK56957	Human secreted pro
C 841	14	7, 7	583	22	ABK62779	Human foetal liver	C 914	14	7, 7	703	24	ABK631572	Human eosinophil-m
C 842	14	7, 7	583	22	ABK31072	Probe #8538 for ge	C 915	14	7, 7	704	22	AA196882	Human neuroblastom
C 843	14	7, 7	583	22	AAK36984	Human brain expres	C 916	14	7, 7	705	20	AAZ15444	Human gene express
C 844	14	7, 7	583	22	AAK36984	Human brain expres	C 917	14	7, 7	708	14	AAQ368098	Xpnt-3all beta-cas
C 845	14	7, 7	583	22	AA117826	Probe #7759 for ge	C 918	14	7, 7	708	14	AAQ368098	Sequence encoding
C 846	14	7, 7	583	24	AAK50991	Probe #1182 used t	C 919	14	7, 7	708	19	AAK35351	Human beta-casain
C 847	14	7, 7	583	24	AAK50991	Human prostate exp	C 920	14	7, 7	708	19	AAK35351	Human beta-casain
C 848	14	7, 7	583	24	AAK50991	Borrelia burgdorfe	C 921	14	7, 7	711	24	AAK57445	Human colon cancer
C 849	14	7, 7	583	20	AAK30814	Rat progression re	C 922	14	7, 7	715	24	AAK562101	Porcine muscular s
C 850	14	7, 7	593	22	AAK31477	Human olfactory re	C 923	14	7, 7	716	20	AAZ17556	Human gene express
C 851	14	7, 7	593	22	AAK32499	Human olfactory re	C 924	14	7, 7	720	24	AAK562104	Porcine muscular s
C 852	14	7, 7	596	22	ABK63031	Human foetal liver	C 925	14	7, 7	721	16	AA135105	Down-regulated sen
C 853	14	7, 7	596	22	AAK30291	Probe #8757 for ge	C 926	14	7, 7	724	22	AA196906	Human neuroblastom
C 854	14	7, 7	596	22	AAK30291	Probe #1749 for ge	C 927	14	7, 7	726	22	AA196906	Human neuroblastom
C 855	14	7, 7	596	22	AA143063	Probe #1749 for ge	C 928	14	7, 7	726	22	AA196906	Human neuroblastom
C 856	14	7, 7	596	24	ABK51222	Human prostate exp	C 929	14	7, 7	728	22	AAK631925	Human immune/haema
C 857	14	7, 7	597	23	ABV51669	Human genome-deriv	C 930	14	7, 7	728	22	ABK51412	Human colon cancer
C 858	14	7, 7	599	19	AAV43880	Mycobacterial meth	C 931	14	7, 7	732	21	AAK64071	Human potaesium ch
C 859	14	7, 7	599	22	ABK62429	Human foetal liver	C 932	14	7, 7	732	21	AAK64071	Human potaesium ch
C 860	14	7, 7	599	22	ABK62429	Human foetal liver	C 933	14	7, 7	732	21	AAK64071	Human potaesium ch
C 861	14	7, 7	599	22	ABK62429	Human foetal liver	C 934	14	7, 7	732	21	AAK64071	Human potaesium ch
C 862	14	7, 7	599	22	AAK14728	Genomic c sequence #	C 935	14	7, 7	732	21	AAK64071	Human potaesium ch
C 863	14	7, 7	599	22	AAK16644	Human bone expres	C 936	14	7, 7	732	21	AAK64071	Human potaesium ch
C 864	14	7, 7	599	22	AAK17498	Human bone expres	C 937	14	7, 7	732	21	AAK64071	Human potaesium ch
C 865	14	7, 7	599	22	AAK142408	Probe #7431 for ge	C 938	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 866	14	7, 7	599	22	AAK10642	Human genome-deriv	C 939	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 867	14	7, 7	600	22	AAK639192	Human cancer relat	C 940	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 868	14	7, 7	600	22	AAK639192	Human cancer relat	C 941	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 869	14	7, 7	600	22	AAK639192	Human cancer relat	C 942	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 870	14	7, 7	604	22	AAK75620	Human polynucleoti	C 943	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 871	14	7, 7	604	22	AAK75620	Human immune/haema	C 944	14	7, 7	732	21	AAK64071	Human KNE2 mutant
C 872	14	7, 7	605	23	ABK32602	Human prostate exp	C 945	14	7, 7	740	24	AAK61964	Porcine muscular s
C 873	14	7, 7	605	23	ABK32602	Human prostate exp	C 946	14	7, 7	741	21	AAK57592	Arabidopsis thalia
C 874	14	7, 7	609	24	ABK68124	Streptococcus poly	C 947	14	7, 7	747	22	AA197344	Human neuroblastom
C 875	14	7, 7	610	24	ABK62626	Rat sequence diffe	C 948	14	7, 7	747	22	AAK573158	DNA encoding novel
C 876	14	7, 7	611	24	ABK62626	Human ovarian anti	C 949	14	7, 7	749	24	ABQ54317	Arabidopsis thalia
C 877	14	7, 7	621	24	AAK35525	Human ovarian anti	C 950	14	7, 7	750	24	ABN70596	Streptococcus poly
C 878	14	7, 7	626	22	AAK35525	DNA encoding nove	C 951	14	7, 7	751	22	AAK505900	Streptococcus poly
C 879	14	7, 7	626	22	AAK35525	Human prostate exp	C 952	14	7, 7	754	22	AAK505900	Human reproductive
C 880	14	7, 7	637	24	ABV46531	Human prostate exp	C 953	14	7, 7	754	22	ABK59464	Human testicular a
C 881	14	7, 7	637	24	ABK59464	Human colon cancer	C 954	14	7, 7	754	22	ABK59464	Human testicular a
C 882	14	7, 7	637	24	AAK20950	Nucleotide sequenc	C 955	14	7, 7	755	22	AAK18837	Human ovarian tumo
C 883	14	7, 7	636	22	AAH77918	Polynucleotide seq	C 956	14	7, 7	759	22	AAH7152	C glutamic codin
C 884	14	7, 7	637	23	ABK34646	Human prostate exp	C 957	14	7, 7	761	20	AAZ15749	Human gene express
C 885	14	7, 7	637	23	ABK34646	Human prostate exp	C 958	14	7, 7	761	20	AAZ15749	Human validated ca

959 14 7.7 765 24 ABN69768 Streptococcus poly
 c 960 14 7.7 768 22 AA197633 Human neuroblastom
 961 14 7.7 769 22 AA124801 Human breast cancer
 c 962 14 7.7 771 24 AA52012 Porcine muscular s
 963 14 7.7 772 24 AA52012 Porcine muscular s
 c 964 14 7.7 779 21 AA297278 Human prostate can
 965 14 7.7 781 24 AA527095 Porcine muscular s
 c 966 14 7.7 783 22 AAH07079 Human cDNA clone (s
 c 967 14 7.7 784 24 AA561903 Porcine muscular s
 968 14 7.7 785 20 AA574119 Rat U3 gene trap d
 c 969 14 7.7 787 22 AA197250 Human neuroblastom
 c 970 14 7.7 789 20 AA217435 Human gene express
 c 971 14 7.7 790 20 AA217435 Human gene express
 c 972 14 7.7 803 24 AA561925 Porcine muscular s
 c 973 14 7.7 804 23 AA555851 Streptococcus pneu
 c 974 14 7.7 810 20 AA217059 Human gene express
 c 975 14 7.7 811 21 AA297258 Human prostate can
 c 976 14 7.7 814 22 AA186468 Human breast cancer
 c 977 14 7.7 818 22 AAH07537 Human cDNA clone (s
 c 978 14 7.7 819 24 AA524143 Porcine muscular s
 c 979 14 7.7 820 24 AA524143 Porcine muscular s
 c 980 14 7.7 831 21 AA555363 Streptococcus aur
 c 981 14 7.7 832 22 AAAL01738 Human reproductive
 c 982 14 7.7 836 23 ABEL97031 Human testicular a
 c 983 14 7.7 837 21 AA297338 Human prostate can
 984 14 7.7 838 24 ABQ68558 Listeria monocytog
 985 14 7.7 838 24 ABQ70294 Bovine interleukin
 c 986 14 7.7 840 26 AA507594 Human cDNA clone (s
 987 14 7.7 840 26 AA507594 Human validated ca
 c 988 14 7.7 843 20 AAAX9680 Human ovarian tumo
 c 989 14 7.7 856 20 AA277501 Streptococcus poly
 c 990 14 7.7 858 24 ABN71103 Human cDNA clone (s
 c 991 14 7.7 863 22 AAH08135 Corynebacterium gl
 c 992 14 7.7 867 22 AA171319 Bovine male enhanc
 993 14 7.7 871 16 AAQ79137 Arabidopsis thalia
 c 994 14 7.7 885 22 AA563699 Bacillus lichenifo
 c 995 14 7.7 891 24 AA574081 DNA encoding novel
 c 996 14 7.7 894 21 AA564319 Streptococcus poly
 c 997 14 7.7 897 24 AA568564 Oligonucleotide fo
 c 998 14 7.7 899 24 ABQ34104 Oligonucleotide fo
 c1000 14 7.7 899 24 ABQ34105

ALIGNMENTS

RESULT 1
 AA124432
 ID AA124432 standard; DNA; 372 BP.
 AC AA124432;
 AC AA124432;
 DT 12-OCT-2001 (first entry)
 DE Probe #14365 for gene expression analysis in human cervical cell sample.
 DE XX Probe; human; microarray; gene expression; cervical epithelial cell;
 DE XX cervical cancer; sb.
 DE XX Homo sapiens.
 OS Homo sapiens.
 PN WO200157278-A2.
 PD PD
 PD 09-AUG-2001.
 PP 30-JAN-2001; 2001WO-US00670.
 PP XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 30-JUN-2000; 2000US-0623366.
 PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PR (MOLB-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 XX Claim 25; SEQ ID No 14365; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human Hela cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging
 CC cancer. The sequence data for this patent did not form part of the printed
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
 Query Match 100.0%; Score 181; DB 22; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5; 4e-82;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ACTTATCCAAATTTACACAGACGCTGGAAGACGCTTCCGAAGGATTTTATTACTTAT 60
 Db 7 ACTTATCCAAATTTACACAGACGCTGGAAGACGCTTCCGAAGGATTTTATTACTTAT 66
 Qy 61 ATGACGACGCTGGCCGACACACACACACACGCTGACGACAGGCGCTCCGACCAAGTTGAT 120
 Db 67 ATGACGACGCTGGCCGACACACACACACACGCTGACGACAGGCGCTCCGACCAAGTTGAT 126
 Qy 121 GCTGAGAACTTCTACTATGTCATCTGTCCTGACCTCATGGTGATGATTGGAATGTTCTTTC 180
 Db 127 GCTGAGAACTTCTACTATGTCATCTGTCCTGACCTCATGGTGATGATTGGAATGTTCTTTC 186
 Qy 181 A 181
 Db 187 A 187
 RESULT 2
 AA109965
 ID AA109965 standard; DNA; 372 BP.
 AC AA109965;
 AC AA109965;
 DT 09-OCT-2001 (first entry)
 DE Probe #9956 used to measure gene expression in human breast sample.
 DE XX Probe; human; breast disease; breast cancer; development disorder; sb.
 DE XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 OS Homo sapiens.
 PN WO200157270-A2.
 PD PD
 PD 09-AUG-2001.
 PP 29-JAN-2001; 2001WO-US00661.
 PP XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.

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PR 21-SEP-2000; 2000US-0234687.
PR 04-OCT-2000; 2000US-0234687.
PR 04-OCT-2000; 2000US-0234687.
PR 04-OCT-2000; 2000US-0234687.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression
XX in a human breast -
XX Claim 25; SEQ ID No 9956; 322pp; English.
XX The present invention relates to novel single exon nucleic acid probes.
XX The present sequence is one such probe. The probes are useful for
XX hybridizing to a single exon in human breast samples, where the probe
XX hybridizes at high stringency to nucleic acids from human
XX breast. The probes are useful for predicting, diagnosing, grading,
XX staging, monitoring and prognosing diseases of the human breast,
XX particularly those diseases with polygenic aetiology. The diseases
XX include: breast cancers, disorders of development, inflammatory diseases
XX of the breast, fibrocystic changes, proliferative breast disease and
XX non-carcinoma tumours.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained independently of the patent. C format directly from Wipo
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
XX
XX Query Match 100.0%; Score 181; DB 22; Length 372;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-82;
XX Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACTTTATCCAAATTTTCACAGAGCGCTGGAGAGCTCTCCGAGAGGATTTTATTACTTAT 60
XX Db 7 ACTTTATCCAAATTTTCACAGAGCGCTGGAGAGCTCTCCGAGAGGATTTTATTACTTAT 66
XX
XX QY 61 ATGGACAAATTTGGCCCGACAGACACACAGCTGACAGAGGCGCTCCAGCCAAAGTTGAT 120
XX Db 67 ATGGACAAATTTGGCCCGACAGACACACAGCTGACAGAGGCGCTCCAGCCAAAGTTGAT 126
XX
XX QY 121 GCTGAGAACTTCTACTATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
XX Db 127 GCTGAGAACTTCTACTATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
XX
XX QY 181 A 181
XX Db 187 A 187
XX
XX RESULT 3
XX AAS00245
XX ID AAS00245 standard; DNA; 372 BP.
XX AC AAS00245;
XX XC AAS00245;
XX DT 10-MAY-2001 (first entry)
XX DE Human potassium channel regulatory protein, Mink2, DNA sequence.
XX
XX Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
XX angina; asthma; diabetes; renal insufficiency; urinary incontinence;
XX irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..372
XX FT /*tag= a
XX FT /product= "MINK2 potassium channel protein"
XX
XX
XX WO200114403-A1.
XX 01-MAR-2001.
XX 18-AUG-2000; 2000MO-US22799.
XX 20-AUG-1999; 99US-0379201.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX Ficker E, Wible B, Brown AM,
XX WPI; 2001-218424/22.
XX P-PSDB; AAU00215.
XX
XX Novel potassium channel gene termed Mink2 encoding potassium channel
XX regulatory protein, useful for screening compounds that are useful for
XX treating diseases caused by aberrant potassium activity -
XX Claim 1; Fig 9; 39pp; English.
XX The sequence represents the coding sequence of human potassium channel
XX regulatory protein, Mink2. Mink2 sequence is useful for producing a
XX screening of agonistic or antagonistic compounds that are useful for
XX treating diseases caused by aberrant potassium activity, such as human
XX C insufficiency, urinary incontinence, irritable colon, epilepsy,
XX cerebrovascular ischaemia, and autoimmune disease.
XX
XX Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
XX
XX Query Match 100.0%; Score 181; DB 22; Length 372;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-82;
XX Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACTTTATCCAAATTTTCACAGAGCGCTGGAGAGCTCTCCGAGAGGATTTTATTACTTAT 60
XX Db 7 ACTTTATCCAAATTTTCACAGAGCGCTGGAGAGCTCTCCGAGAGGATTTTATTACTTAT 66
XX
XX QY 61 ATGGACAAATTTGGCCCGACAGACACACAGCTGACAGAGGCGCTCCAGCCAAAGTTGAT 120
XX Db 67 ATGGACAAATTTGGCCCGACAGACACACAGCTGACAGAGGCGCTCCAGCCAAAGTTGAT 126
XX
XX QY 121 GCTGAGAACTTCTACTATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
XX Db 127 GCTGAGAACTTCTACTATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
XX
XX QY 181 A 181
XX Db 187 A 187
XX
XX RESULT 4
XX ABA44797
XX ID ABA44797 standard; DNA; 450 BP.
XX AC ABA44797;
XX XC ABA44797;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #3492.
XX
XX Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer; se.
XX
XX Homo sapiens.
XX
XX WO200157271-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00662.

```


KW Cardiovascular disease; hypertension; cardiac arrhythmia;
 KW Congenital heart disease; as.
 XX Homo sapiens.

OS W0200157274-A2.
 PN W0200157274-A2.
 XX 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US00666.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-48899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX Claim 1; SEQ ID No 3463; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC probes are sequenced and the probes may be used to measure gene expression
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC record of the patent and is not in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 181; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTCCACACAGCGCTGCGAAGAGCTCTTCGAGAGATTTTATTACTTAT 60
 Db 162 ACTTTATCCAAATTTCCACACAGCGCTGCGAAGAGCTCTTCGAGAGATTTTATTACTTAT 221
 Qy 61 ATGGACAATTTGGCCGACACACACAGCTGAGCAGAGAGCCCTCCAGCCAAAGTTGAT 120
 Db 222 ATGGACAATTTGGCCGACACACACAGCTGAGCAGAGAGCCCTCCAGCCAAAGTTGAT 281
 Qy 121 GCTGAGACTTCTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 180
 Db 282 GCTGAGACTTCTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 341
 Qy 181 A 181
 Db 342 A 342

RESULT 7
 AAK03508
 ID AAK03508 standard; DNA; 450 BP.

XX AAK03508;
 XX 05-NOV-2001 (first entry)

DT

XX Human brain expressed single exon probe SEQ ID NO: 3499.
 XX Homo sapiens.
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW Microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW Epilepsy; cancer; as.
 XX Homo sapiens.
 OS W0200157275-A2.
 PN W0200157275-A2.
 XX 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US00667.
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483446/52.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -

XX Example 4; SEQ ID NO: 3499; 650pp + Sequence Listing; English.
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.

XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 181; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTCCACACAGCGCTGCGAAGAGCTCTTCGAGAGATTTTATTACTTAT 60
 Db 162 ACTTTATCCAAATTTCCACACAGCGCTGCGAAGAGCTCTTCGAGAGATTTTATTACTTAT 221
 Qy 61 ATGGACAATTTGGCCGACACACACAGCTGAGCAGAGAGCCCTCCAGCCAAAGTTGAT 120
 Db 222 ATGGACAATTTGGCCGACACACACAGCTGAGCAGAGAGCCCTCCAGCCAAAGTTGAT 281
 Qy 121 GCTGAGACTTCTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 180
 Db 282 GCTGAGACTTCTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 341
 Qy 181 A 181
 Db 342 A 342

RESULT 8
 AAK28962
 ID AAK28962 standard; DNA; 450 BP.

XX AAK28962;
 XX 06-NOV-2001 (first entry)

DT

DE Human bone marrow expressed single exon probe SEQ ID NO: 3519.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 XX WO200157276-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00670.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 03-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0234687.
 XX 21-SEP-2000; 2000US-0236359.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 DR analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 3519; 559pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of
 CC the probes of the invention.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 SQ Query Match 100.0%; Score 181; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. NO. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTTATCCAAATTTCCACAGAGCGCTTCCGAGAGCTTTTATCTACTTAT 60
 DB 162 ACTTTATCCAAATTTCCACAGAGCGCTTCCGAGAGCTTTTATCTACTTAT 221
 QY 61 ATGACAAATTTGGCCGACACAGACAGCTGAGCAGAGGCGCTTCGAGCAAGTTGAT 120
 DB 222 ATGACAAATTTGGCCGACACAGACAGCTGAGCAGAGGCGCTTCGAGCAAGTTGAT 281
 QY 121 GCTGAGAACTTCTACTATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 282 GCTGAGAACTTCTACTATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 341
 QY 181 A 181
 DB 342 A 342
 RESULT 9
 AA113549
 ID AA113549 standard; DNA; 450 BP.
 XX AA113549;
 XX AA113549;
 XX 12-OCT-2001 (first entry)
 DE Probe #3482 for gene expression analysis in human cervical cell sample.
 XX Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer; ss.
 XX Homo sapiens.
 XX WO200157276-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00670.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 03-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0234687.
 XX 21-SEP-2000; 2000US-0236359.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 DR analyzing gene expression in human cervical epithelial cells -
 XX Claim 25; SEQ ID No 3482; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human Hela cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging
 CC of diseases of the cervix, notably cervical cancer. A portion of the printed
 CC specification, but was obtained in electronic format directly from NIPO
 CC at fcp.wipo.int/pub/published_pct_sequences.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 SQ Query Match 100.0%; Score 181; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. NO. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTTATCCAAATTTCCACAGAGCGCTTCCGAGAGCTTTTATCTACTTAT 60
 DB 162 ACTTTATCCAAATTTCCACAGAGCGCTTCCGAGAGCTTTTATCTACTTAT 221
 QY 61 ATGACAAATTTGGCCGACACAGACAGCTGAGCAGAGGCGCTTCGAGCAAGTTGAT 120
 DB 222 ATGACAAATTTGGCCGACACAGACAGCTGAGCAGAGGCGCTTCGAGCAAGTTGAT 281
 QY 121 GCTGAGAACTTCTACTATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 282 GCTGAGAACTTCTACTATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 341
 QY 181 A 181
 DB 342 A 342
 RESULT 10
 AA134911
 ID AA134911 standard; DNA; 450 BP.
 XX AA134911;
 XX AA134911;
 XX 17-OCT-2001 (first entry)
 DE Probe #3597 used to measure gene expression in human placenta sample.
 XX Probe; human; microarray; gene expression; cervical epithelial cell;

CC expression, the probes are therefore useful in grading and/or staging
 CC of this cancer, and are therefore useful in grading and/or staging
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
 Query Match 100.0%; Score 181; DB 22; Length 471;
 Best Local Similarity 100.0%; Pred. No. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTACACAGAGCGCTGGAGAGCTCTCCGAAGGATTTTATTACTTAT 60
 Db 245 ACTTTATCCAAATTTACACAGAGCGCTGGAGAGCTCTCCGAAGGATTTTATTACTTAT 304

Oy 61 ATGACAAATTTGGCCGACAGACAGACAGAGCGCTCCGAGAGATTTTATTACTTAT 120
 Db 305 ATGACAAATTTGGCCGACAGACAGACAGAGCGCTCCGAGAGATTTTATTACTTAT 364

Oy 121 GGTGAGAACTTCTACTATGTATGTCCTGTACTCTATGGTGATGATGGAATGTTCTCTTC 180
 Db 365 GGTGAGAACTTCTACTATGTATGTCCTGTACTCTATGGTGATGATGGAATGTTCTCTTC 424

Oy 181 A 181
 Db 425 A 425

RESULT 14
 AA104990
 ID AA104990 standard; DNA; 471 BP.
 XX AC AA104990;
 DT 09-OCT-2001 (first entry)
 XX Probe #4981 used to measure gene expression in human breast sample.
 XX Probe; human; breast disease; breast cancer; development disorder; ss;
 XX inflammatory disease; Proliferative breast disease; non-carcinoma tumour.
 XX Homo sapiens.
 XX WO200157270-A2.
 XX 09-AUG-2001.
 XX 29-JAN-2001; 2001WO-US00661.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0609408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0216359.
 XX 04-OCT-2000; 2000US-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-476286/S1.
 XX Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -
 XX Claim 25; SEQ ID No 4981; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes.
 XX The present sequence is one such probe. The probes are useful for
 XX measuring human gene expression in a human breast sample, where the probe
 XX hybridises at high stringency to a nucleic acid expressed in the human

CC breast. The probes are useful for predicting, diagnosing, grading,
 CC staging, monitoring and prognosticating diseases and human diseases
 CC including, but not limited to, cancer, and other diseases. The diseases
 CC include: breast cancer; disorders of development; inflammatory diseases
 CC of the breast; fibrocystic changes; proliferative breast disease and
 CC non-carcinoma tumours.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
 Query Match 100.0%; Score 181; DB 22; Length 471;
 Best Local Similarity 100.0%; Pred. No. 5.4e-82;
 Matches 181; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTACACAGAGCGCTGGAGAGCTCTCCGAAGGATTTTATTACTTAT 60
 Db 245 ACTTTATCCAAATTTACACAGAGCGCTGGAGAGCTCTCCGAAGGATTTTATTACTTAT 304

Oy 61 ATGACAAATTTGGCCGACAGACAGACAGAGCGCTCCGAGAGATTTTATTACTTAT 120
 Db 305 ATGACAAATTTGGCCGACAGACAGACAGAGCGCTCCGAGAGATTTTATTACTTAT 364

Oy 121 GGTGAGAACTTCTACTATGTATGTCCTGTACTCTATGGTGATGATGGAATGTTCTCTTC 180
 Db 365 GGTGAGAACTTCTACTATGTATGTCCTGTACTCTATGGTGATGATGGAATGTTCTCTTC 424

Oy 181 A 181
 Db 425 A 425

RESULT 15
 AAF80269
 ID AAF80269 standard; DNA; 471 BP.
 XX AC AAF80269;
 DT 29-JUN-2001 (first entry)
 XX Nucleotide sequence of human potassium channel subunit Isk2.
 XX Human; potassium channel; Isk2; gene therapy; gastric motility;
 XX gastric acid secretion; anti-arrhythmic agent; myocardial infarction; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS position 7450
 XX Feature Key
 XX /product= "potassium channel subunit Isk2"
 XX WO200127246-A1.
 XX 19-APR-2001.
 XX 10-OCT-2000; 2000WO-US28014.
 XX 12-OCT-1999; 99US-0158781.
 XX (MERI) MERCK & CO INC.
 XX Swanson RJ, Liu Y, Folander K;
 XX WPI; 2001-273764/28.
 XX P-PSDB; AAB67800.
 XX New DNA encoding the Isk2 potassium channel subunit, useful e.g. for
 XX detecting mutations and screening for therapeutic agents -
 XX Claim 3; Fig 1A; 46pp; English.

PS Claim 17; Page 162-163; 164pp; English.

XX The invention relates to identifying (M1) a compound that modulates

CC biological activity of a potassium channel (PC), by contacting a

CC compound with a structure comprising a PC polypeptide and a polypeptide

CC cloned from a rat cerebellar cDNA library (KCRI), and determining the

CC activity of the PC polypeptide in the presence and absence of the

CC compound, where a difference in the activities indicates modulation of

CC biological activity of PC. Also include are identifying (M2) a candidate

CC compound, where a difference in the activities indicates modulation of

CC biological activity of PC. Also include are identifying (M3) a candidate

CC human ether-a-go-go-related gene (HERG) channel polypeptide and KCRI

CC polypeptide, identifying (M4) a candidate compound as a modulator of KCRI

CC expression, modulating (M4) PC function in a subject, comprising

CC administering to the subject a substance that provides expression of a

CC KCRI-encoding nucleic acid molecule in a cell or tissue, where modulated

CC PC function is desired, screening (M5) for susceptibility to a drug-

CC resistant cardiac arrhythmia in a subject, comprising obtaining a

CC biological sample from the subject, identifying (M6) a KCRI gene

CC gene in the biological sample from the subject, where the presence of the

CC polymorphism indicates the susceptibility of the subject to a

CC drug-induced cardiac arrhythmia, an oligonucleotide pair, where a first

CC oligonucleotide of the pair hybridises to a first portion of a KCRI gene

CC which includes a polymorphism of the KCRI gene, and the second

CC oligonucleotide of the pair hybridises to a second portion of the KCRI

CC oligonucleotide adjacent to the first portion and a set of antisense

CC oligonucleotides adjacent to the first portion, identifying (M7) a KCRI gene

CC which includes a polymorphism of the KCRI gene (M1) is useful for

CC identifying a compound that modulates biological activity of PC,

CC especially HERG, for modulating PC function (i.e. modulating HERG

CC activity) in a mammal, by preparing a composition comprising the

CC compound and administering the composition. The compound is useful for

CC treating or preventing long QT syndrome (LQT) and is useful in drug

CC protein. The present sequence encodes a HERG interacting

CC protein Mirp1 (not defined).

XX

SQ Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

Query Match 100.0%; Score 181; DB 24; Length 732;

Best Local Similarity 100.0%; Pred. No. 5.5e-82;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTCCACAGAGCGCTGGAGACGCTCTCGAAGAGATTTTATTACTTAT 60

Db 80 ACTTTATCCAAATTTCCACAGAGCGCTGGAGACGCTCTCGAAGAGATTTTATTACTTAT 139

Oy 61 ATGGACAATTTGGCGCCAGACACACACAGCTGACGAAGAGCGCTCCAGAGCCAAAGTTGAT 120

Db 140 ATGGACAATTTGGCGCCAGACACACACAGCTGACGAAGAGCGCTCCAGAGCCAAAGTTGAT 199

Oy 121 GCTGAGAACTTCTACTATGTATCTCTGATCTCTGATCTCTGATCTCTGATCTCTCTTC 180

Db 200 GCTGAGAACTTCTACTATGTATCTCTGATCTCTGATCTCTGATCTCTGATCTCTCTTC 259

Oy 181 A 181

Db 260 A 260

RESULT 21

AAD35169

ID AAD35169 standard; DNA; 732 BP.

XX AAD35169;

DT 25-JUL-2002 (first entry)

XX Human KCNE2 mutant DNA (C420T).

DE Human KCNE2 related ion channel protein; Mirp1; ion channel disorder;

XX KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;

KW single nucleotide polymorphism; ds.

XX

CS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 74..445

FT /tag= a

FT /product= "Human Mirp1 mutant protein"

FT /replace (420, C)

FT /tag= b

FT /standard_name= "single nucleotide polymorphism (SNP)"

XX NC0200222875-A2.

XX 21-MAR-2002.

XX 11-SEP-2001; 2001WO-US28332.

XX 11-SEP-2000; 2000US-231571P.

XX (UYUA) UNIV YALE.

XX Goldstein SAN;

PI WPI; 2002-362360/39.

DR P-PSDB; AAE22094.

XX Novel gene encoding Min-K related ion channel protein subunit and

XX polymorphisms in this gene associated with antibiotic-induced long QT

XX syndrome.

PS Claim 1; Page 41-42; 49pp; English.

XX The present invention relates to novel KCNE2 genes encoding Min-K related

CC (Mirp) 1 ion channel proteins and polymorphisms in these genes that are

CC associated with ion channel disorders including antibiotic-induced long

CC QT syndrome and cardiac arrhythmia. The present sequence encodes a

CC 57 or 116 of Mirp1 polypeptide or a mutation at a nucleotide position

CC encoding the amino acid positions is useful for diagnosing the presence

CC of a polymorphism that causes drug-induced LQTS. The diagnostic methods

CC are useful in the development of new drug therapies which selectively

CC target one or more KCNE2 polymorphisms that are associated with cardiac

CC arrhythmias. The present sequence is human KCNE2 mutant DNA (C420T).

XX

SQ Sequence 732 BP; 221 A; 151 C; 157 G; 203 T; 0 other;

Query Match 100.0%; Score 181; DB 24; Length 732;

Best Local Similarity 100.0%; Pred. No. 5.5e-82;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTCCACAGAGCGCTGGAGACGCTCTCGAAGAGATTTTATTACTTAT 60

Db 80 ACTTTATCCAAATTTCCACAGAGCGCTGGAGACGCTCTCGAAGAGATTTTATTACTTAT 139

Oy 61 ATGGACAATTTGGCGCCAGACACACACAGCTGACGAAGAGCGCTCCAGAGCCAAAGTTGAT 120

Db 140 ATGGACAATTTGGCGCCAGACACACACAGCTGACGAAGAGCGCTCCAGAGCCAAAGTTGAT 199

Oy 121 GCTGAGAACTTCTACTATGTATCTCTGATCTCTGATCTCTGATCTCTGATCTCTCTTC 180

Db 200 GCTGAGAACTTCTACTATGTATCTCTGATCTCTGATCTCTGATCTCTGATCTCTCTTC 259

Oy 181 A 181

Db 260 A 260

RESULT 22

AAD35170

ID AAD35170 standard; DNA; 732 BP.

XX AAD35170;

DT 25-JUL-2002 (first entry)

XX Human KCNE2 wild type DNA.

XX Human; Min-K related ion channel protein; MIRP1; ion channel disorder;
 XX KNCN2; long QT syndrome; LQTS; cardiac arrhythmia; gene; db.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 74..445
 XX /*tag= a
 XX /product= "Human MIRP1 protein"
 XX
 XX WO200222875-A2.
 XX
 XX 21-MAR-2002.
 XX
 XX 11-SEP-2001; 2001WO-US28332.
 XX
 XX 11-SEP-2000; 2000US-231571P.
 XX
 XX (UYUA) UNIV YALE.
 XX Goldstein SAN;
 XX
 XX WPI; 2002-362360/39.
 XX P-PSDB; AAE22095.
 XX
 XX Novel gene encoding Min-K related ion channel protein subunit and
 XX polymorphisms in this gene associated with antibiotic-induced long QT
 XX syndrome -
 XX
 XX Claim 9; Page 43; 49pp; English.
 XX
 XX The present invention relates to novel KNCN2 genes encoding Min-K related
 XX (MIRP1) ion channel proteins and polymorphisms in these genes that are
 XX associated with ion channel disorders including antibiotic-induced long
 XX QT syndrome (LQTS). Detecting a mutation at amino acid positions 54,
 XX 57, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78,
 XX 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97,
 XX 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112,
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 XX 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141,
 XX 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
 XX 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169,
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 XX 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127,
 XX 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139,
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 XX 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187,
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 XX 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823,
 XX 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835,
 XX 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847,
 XX 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859,
 XX 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871,
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 XX 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895,
 XX 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907,
 XX 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919,
 XX 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931,
 XX 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943,
 XX 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955,
 XX 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967,
 XX 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979,
 XX 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991,
 XX 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003,
 XX 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015,
 XX 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027,
 XX 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039,
 XX 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051,
 XX 2052, 2053, 2054, 2

Qy 137 ATGTCATCTCTGACCTCATGTGATGATTCGGAATGTCCTCTTCA 181
 Db 216 ATGTCATCTCTGACCTCATGTGATGATTCGGAATGTCCTTCA 260

RESULT 24

AD35173 standard; DNA; 732 BP.
 ID AAD35173;
 AC AAD35173;
 DT 25-JUL-2002 (first entry)
 XX Human KCNE2 mutant DNA (A95G).
 DE Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
 KW KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
 XX single nucleotide polymorphism; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 74..445
 FT /tag: a
 FT /tag: b
 FT /replace (95, A)
 FT /*tag: b
 FT /standard_name= "Single nucleotide polymorphism (SNP) "
 XX W0200222875-A2.
 XX 21-MAR-2002.
 XX 11-SEP-2001; 2001WO-US28332.
 XX 11-SEP-2000; 2000US-231571P.
 XX (UYVA) UNIV YALE.
 XX Goldstein SN;
 XX WPI: 2002-362360/39.
 XX P-PSDB: A4522098.
 XX Novel gene encoding Min-K related ion channel protein subunit and
 XX polymorphisms in this gene associated with antibiotic-induced long QT
 XX syndrome -
 XX Claim 18; Page 47-48; 49pp; English.

XX The invention relates to novel KCNE2 genes encoding Min-K related
 CC (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
 CC associated with ion channel disorders including antibiotic-induced long
 CC QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
 CC 57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
 CC encoding the amino acid positions is useful for diagnosing the presence
 CC of the genetic defect in LQTS. The diagnostic methods
 CC are useful in the development of new drugs that
 CC target one or more KCNE2 polymorphisms that are associated with cardiac
 CC arrhythmias. The present sequence is human KCNE2 mutant DNA (A95G).
 XX Sequence 732 BP; 220 A; 152 C; 158 G; 202 T; 0 other;

Query Match 91.2%; Score 165; DB 24; Length 712;
 Best Local Similarity 100.0%; P-Value 2.1e-74;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CACAGAGCGTCGGAAGCGTCTCCGAGAGATTTTATTACTATATGCAATGGCGCC 76
 Db 96 CACAGAGCGTCGGAAGCGTCTCCGAGAGATTTTATTACTATATGCAATGGCGCC 155
 Qy 77 AGACACACAGCTGACGACGAGCGCTCCACGCCAAAGTGTGCTGAGAACTTCTACT 136

Db 156 AGACACACAGCTGACGACGAGCGCTCCACGCCAAAGTGTGCTGAGAACTTCTACT 215
 Qy 137 ATGTCATCTCTGACCTCATGTGATGATTCGGAATGTCCTCTTCA 181
 Db 216 ATGTCATCTCTGACCTCATGTGATGATTCGGAATGTCCTTCA 260

RESULT 25

NC64085
 ID AAC64085 standard; DNA; 732 BP.
 XX AAC64085;
 DT 19-FEB-2001 (first entry)
 XX Human potassium channel protein KCNE2 (MiRP1) I57T mutant DNA.
 DE Human; KCNE2; MiRP1; potassium channel protein; KCNE1-related;
 KW Human-related; long QT syndrome; cardiac arrhythmia;
 XX drug screening; knockout mouse; transgenic animal; ion channel disorder;
 KW fast delayed rectifier potassium channel; anti-KCNE2 antibody;
 XX HERG; mutant; ds.
 OS Homo sapiens.
 OS Synchetic.
 PN W0200063434-A1.
 XX 26-OCT-2000.
 XX 14-APR-2000; 2000WO-US10004.
 XX 15-APR-1999; 99US-0139404.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX (UYVA) UNIV YALE.
 XX Abbott GW, Seeti F, Splawski I, Keating MT, Goldstein SAN;
 XX WPI: 2000-672747/65.
 XX P-PSDB: AAB29595.
 XX Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
 XX diagnosing and treating ion channel disorders, especially long QT
 XX syndrome -
 XX Claim 56; Page -; 132pp; English.

XX The invention relates to novel ion channel proteins related to
 CC KCNE1 (MiRP1) and KCNE2 (MiRP2). The invention is directed to the
 CC the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
 CC respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
 CC respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
 CC respectively). The cDNAs encoding these proteins are given in AAC64071-
 CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
 CC potassium channels (I_{Kr}), mutations in which are associated with long
 CC QT syndrome. The invention also relates to methods of diagnosing long QT
 CC syndrome using the genes encoding KCNE2, KCNE3, KCNE4 and KCNE5
 CC disruption in endoplasmic reticulum. KCNE2, KCNE3, KCNE4 and KCNE5
 CC nonhuman animals comprising a heterologous ion channel protein gene
 CC of the invention, a transgenic animal comprising human KCNE2 and HERG
 CC DNA, and methods of and screening drugs for treating long QT syndrome
 CC using KCNE2 proteins (including mutants), nucleic acids encoding them
 CC and antibodies against KCNE2 proteins. The methods, antibodies, nucleic
 CC acids, and proteins may be used for diagnosing or treating ion channel
 CC disorders. The invention also relates to methods of diagnosing long QT
 CC KCNE2 and HERG are useful for testing anti-QT syndrome drugs.
 CC The present sequence represents DNA encoding a mutant human KCNE2
 CC (MiRP1) specifically claimed for use in diagnostic and drug screening
 CC methods of the invention.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the wild-type human KCNE2 cDNA sequence shown on page

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CC 118-119.
XX Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
SQ

Query Match          90.1%; Score 163; DB 21; Length 732;
Best Local Similarity 100.0%; Pred. No. 7.3e-73;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTCCACAGAGCTGGAAGAGCTCTTCGAGAGATTTTACTTAT 60
Db 80 ACTTTATCCAAATTTCCACAGAGCTGGAAGAGCTCTTCGAGAGATTTTACTTAT 139
Oy 61 ATGAGCAATTTGGCGGCGAGACACACAGCTGAGCAAGAGCTCTCAAGCCAAAGTTGAT 120
Db 140 ATGAGCAATTTGGCGGCGAGACACACAGCTGAGCAAGAGCTCTCAAGCCAAAGTTGAT 199
Oy 121 GCTGAGAACTTCTACTATGTCATCTGTCATCTCATGCTGATGA 163
Db 200 GCTGAGAACTTCTACTATGTCATCTGTCATCTCATGCTGATGA 242

RESULT 26
AD35172
ID AAD35172 standard; DNA; 732 BP.
XX AAC64083
AC AAC64083;
AT 19-FEB-2001 (first entry)
DT
DX
DY
DE Human KCNE2 mutant DNA (T243C).
XX
KW Human; Min-K related ion channel protein; MIRP1; ion channel disorder;
KW KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
EN Key Location/Qualifiers
XX 74..445
XX CDS
XX
FT variation
FT /product= "Human MIRP1 mutant protein"
FT replace (243, T)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
XX WQ200222875-A2.
XX
XX PD 21-MAR-2002.
XX
XX PF 11-SEP-2001; 2001MO-US28332.
XX
XX PR 11-SEP-2000; 2000US-231571P.
XX
XX PX (UYUA ) UNIV YALE.
XX
XX PI Goldstein SAN;
XX
XX DR WPI; 2002-362360/39.
XX
XX DR P-PSDB; AAB22097.
XX
XX Novel gene encoding Min-K related ion channel protein subunit and
XX polymorphisms in this gene associated with antibiotic-induced long QT
XX syndrome -
XX
XX PS Claim 15; Page 46; 49pp; English.
XX
XX The present invention relates to novel KCNE2 genes encoding Min-K related
XX (MIRP1) ion channel proteins and polymorphisms in these genes that are
XX associated with long QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
XX 57 or 116 of MIRP1 polypeptide or a mutation at a nucleotide position
XX encoding the amino acid positions is useful for diagnosing the presence
XX of a polymorphism that causes drug-induced LQTS. The diagnostic methods

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are useful in the development of new drug therapies which selectively
CC target one or more KCNE2 polymorphisms that are associated with cardiac
CC arrhythmias. The present sequence is human KCNE2 mutant DNA (T243C).
XX
SQ Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
XX
Query Match          90.1%; Score 163; DB 24; Length 732;
Best Local Similarity 100.0%; Pred. No. 7.3e-73;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTTATCCAAATTTCCACAGAGCTGGAAGAGCTCTTCGAGAGATTTTACTTAT 60
Db 80 ACTTTATCCAAATTTCCACAGAGCTGGAAGAGCTCTTCGAGAGATTTTACTTAT 139
Oy 61 ATGAGCAATTTGGCGGCGAGACACACAGCTGAGCAAGAGCTCTCAAGCCAAAGTTGAT 120
Db 140 ATGAGCAATTTGGCGGCGAGACACACAGCTGAGCAAGAGCTCTCAAGCCAAAGTTGAT 199
Oy 121 GCTGAGAACTTCTACTATGTCATCTGTCATCTCATGCTGATGA 163
Db 200 GCTGAGAACTTCTACTATGTCATCTGTCATCTCATGCTGATGA 242

RESULT 27
AAC64083
ID AAC64083 standard; DNA; 732 BP.
XX AAC64083;
AT 19-FEB-2001 (first entry)
DT
DX
DY
DE Human potassium channel protein KCNE2 (MIRP1) Q9E mutant DNA.
XX
KW Human; KCNE2; MIRP1; potassium channel protein; KCNE1-related;
KW Min-K-related; long QT syndrome; cardiac arrhythmia;
KW drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW delayed rectifier potassium channel; anti-KCNE2 antibody;
KW HERG; mutant; ds.
XX
OS Homo sapiens.
XX
EN Key Location/Qualifiers
XX 74..445
XX CDS
XX
FT variation
FT /product= "Human MIRP1 mutant protein"
FT replace (243, T)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
XX WQ200222875-A2.
XX
XX PD 21-MAR-2002.
XX
XX PF 11-SEP-2001; 2001MO-US28332.
XX
XX PR 11-SEP-2000; 2000US-231571P.
XX
XX PX (UYUA ) UNIV YALE.
XX
XX PI Goldstein SAN;
XX
XX DR WPI; 2000-672747/65.
XX
XX DR P-PSDB; AAB29593.
XX
XX Novel nucleic acids encoding MIRP1, MIRP2 and MIRP3, useful for
XX diagnosing and treating ion channel disorders, especially long QT
XX syndrome -
XX
XX PS Claim 56; Page 7; 132pp; English.
XX
XX The invention relates to novel ion channel proteins related to
XX KCNE1 (MinK) and to nucleic acids encoding them. The proteins of
XX the invention are human and rat KCNE2 (MIRP2), AAB29597 and AAB29598,
XX respectively; and human and mouse KCNE4 (MIRP4), AAB29597 and AAB29598,
XX respectively. The cDNAs encoding these proteins are given in AAC64071-
XX AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
XX potassium channels (I-KR), mutations in which are associated with long QT
XX syndrome. The invention also relates to methods of diagnosing long QT

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PN XX WO200222875-A2.
PD XX
PF XX 21-MAR-2002.
PX XX
PY XX
PZ XX
QA XX 11-SEP-2001; 2001WO-US28332.
QB XX
QC XX 11-SEP-2000; 2001WO-US23171P.
QD XX
QE XX (UYUA ) UNIV VALE.
QF XX
QG XX Goldstein SAN;
QH XX
QI XX WPI; 2002-362360/39.
QJ XX F-RDB; AAE22056.
QK XX
QL XX Novel gene encoding Min-K related ion channel protein subunit and
QM XX polymorphisms in this gene associated with antibiotic-induced long QT
QN XX syndrome -
QO XX
QP XX Claim 12; Page 44-45; 49pp; English.
QR XX The present invention relates to novel KCNE2 genes encoding Min-K related
QS XX (MiRP) ion channel proteins and polymorphisms in these genes that are
QT XX associated with ion channel disorders including antibiotic-induced long
QU XX QT syndrome (LQTS). Detecting a mutation at amino acid position 8, 54,
QV XX 57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
QW XX encoding the amino acid positions is useful for diagnosing the presence
QX XX of a polymorphism that causes drug-induced LQTS. The diagnostic methods
QY XX are useful in the development of new drug therapies which selectively
QZ XX treat or prevent or reduce the risk of secondarily acquired cardiac
RA XX arrhythmias. The present sequence is human KCNE2 mutant DNA (T734C).
RB XX
RC XX Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
RD XX
RE XX Query Match 85.1%; Score 154; DB 24; Length 732;
RF XX Best Local Similarity 100.0%; Pred. No. 2.7e-68;
RG XX Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RH XX
RI XX 1 ACTTTATCCCAATTTTCACAGAGCGTGGAAACAGCTCTTCGAGGATTTTATTACTTAT 60
RJ XX
RK XX 80 ACTTTATCCCAATTTTCACAGAGCGTGGAAACAGCTCTTCGAGGATTTTATTACTTAT 139
RL XX
RM XX 61 ATGAGCAATTCGCCGACAGACACAAACGCTGACGAGAGGCGCTCGAGCCAAAGTTGAT 120
RN XX
RO XX 140 ATGAGCAATTCGCCGACAGACACAAACGCTGACGAGAGGCGCTCGAGCCAAAGTTGAT 199
RP XX
RQ XX 121 GCTGAGAACTTCTACTATGTCATCTGTACTCTCA 154
RS XX
RT XX 200 GCTGAGAACTTCTACTATGTCATCTGTACTCTCA 233
RU XX
RV XX RESULT 30
RW XX ABA49938
RX XX ID: ABA49938 standard; DNA; 312 BP.
RY XX
RZ XX ABA49938;
RA XX
RB XX 01-FEB-2002 (first entry)
RC XX
RD XX Human breast cell single exon nucleic acid probe #8633.
RE XX
RF XX Human; microarray; single exon probe; gene expression; breast;
RG XX disease; cancer; es.
RH XX
RI XX Homo sapiens.
RJ XX
RK XX WO200157271-A2.
RL XX
RM XX 09-AUG-2001.
RN XX
RO XX 30-JAN-2001; 2001WO-US00662.
RP XX
RQ XX 04-FEB-2000; 2000US-0180312.
RS XX

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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0609408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0239329.
04-OCT-2000; 2000US-024265.
(MOLE-) MOLECULAR DYNAMICS INC.
Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-496933/54.
New spatially-addressable set of single exon nucleic acid probes,
useful for measuring gene expression in sample derived from human
breast, comprises number of single exon nucleic acid probes -
Claim 4; SEQ ID NO 8633; 327pp + sequence listing; English.
The invention relates to a spatially-addressable set of single exon
nucleic acid probes useful for measuring gene expression in sample
derived from human breast and B17 cells. The method involves contacting
the probes with a collection of detectably labelled nucleic acids
derived from mRNA of human breast, and then measuring the label
bound to each probe of the microarray. The probes are useful for
verifying the expression of regions of genomic DNA predicted to
encode proteins. They are useful for gene discovery, and for
determining predisposition and/or prognosing breast disease. Gene
expression analysis of human breast tissue using the probes and
agents on cells. The microarray of this invention presents a far greater
diversity of probes for measuring gene expression, with far less bias
than expressed sequence tag microarrays. The method is suitable for
rapid production of functional information from genomic sequence. The
present sequence is a single exon nucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of the
prior art specification, but was obtained from Genbank and deposited
from WFO at ftp://wipo.int/pub/published_pat_sequences.
Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
Query Match 74.0%; Score 134; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 48 TTTTATTACTTATGACATTTGCGCCGAGACACACACAGCTGAGCAAGAGCCCTCCA 107
DB 1 TTTTATTACTTATGACATTTGCGCCGAGACACACACAGCTGAGCAAGAGCCCTCCA 60
OY 108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTCTGACCTGATGATGATTTGG 167
DB 61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTCTGACCTGATGATGATTTGG 120
OY 168 AATGTTCTCTTCA 181
DB 121 AATGTTCTCTTCA 134
RESULT 31
ABA67856
ID: ABA67856 standard; DNA; 312 BP.
AC ABA67856;
AD
AE 01-FEB-2002 (first entry)
AF
AG Human foetal liver single exon nucleic acid probe #16161.
AH Human; foetal liver; gene expression; single exon nucleic acid probe; es.
AI Homo sapiens.
AJ
AK WO200157277-A2.
AL

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PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234697.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000US-0234359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX heart -
XX
XX Claim 4; SEQ ID NO 13379; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX present invention provides a means for predicting, measuring, displaying
XX monitoring and prognosticating diseases of the heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
XX
Query Match 74.0%; Score 134; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 48 TTTTATTACTTATATGACAAATTGGCCGAGACACACAGCTGACGAGGCGCTTCCA 107
Db 1 TTTTATTACTTATATGACAAATTGGCCGAGACACACAGCTGACGAGGCGCTTCCA 60
Oy 108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTGCTACCTCATGTGATGATGG 167
Db 61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTGCTACCTCATGTGATGATGG 120
Oy 168 AATGTCCTCTTCCA 181
Db 121 AATGTCCTCTTCCA 134
RESULT 32
ABA34913
ID ABA34913 standard; DNA; 312 BP.
XX
XX ABA34913;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #13379 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX

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XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234697.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000US-0234359.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX heart -
XX
XX Claim 4; SEQ ID NO 13379; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX present invention provides a means for predicting, measuring, displaying
XX monitoring and prognosticating diseases of the heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
XX
Query Match 74.0%; Score 134; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 48 TTTTATTACTTATATGACAAATTGGCCGAGACACACAGCTGACGAGGCGCTTCCA 107
Db 1 TTTTATTACTTATATGACAAATTGGCCGAGACACACAGCTGACGAGGCGCTTCCA 60
Oy 108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTGCTACCTCATGTGATGATGG 167
Db 61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTGCTACCTCATGTGATGATGG 120
Oy 168 AATGTCCTCTTCCA 181
Db 121 AATGTCCTCTTCCA 134
RESULT 32
ABA34913
ID ABA34913 standard; DNA; 312 BP.
XX
XX ABA34913;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #13379 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX

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PR	27-SEP-2000;	2000US-0236359.
PR	04-OCT-2000;	2000GB-0024263.
XX	(MOLE-) MOLECULAR DYNAMICS INC.	
PA	Penn SG,	Hanzel DK, Chen W, Rank DR;
XX	WPI,	2001-488900/53.
XX	Human genome-derived single exon nucleic acid probes useful for	
PT	analyzing gene expression in human bone marrow -	
XX	Example 4; SEQ ID NO: 16565; 65sepp + Sequence Listing; English.	
XX	The present invention provides a number of single exon nucleic acid	
CC	probes which detect and identify genomic sequences expressed in the human	
CC	bone marrow. They can be used to measure gene expression in bone marrow	
CC	samples, which may enable the improved diagnosis and treatment of cancers	
CC	such as lymphoma, leukemia and myeloma. The present sequence is one of	
CC	the probes of the invention.	
XX	Sequence 312 BP; 94 C; 73 G; 71 A; 74 T; 0 other;	
SQ		
Query Match	74.0%; Score 134; DB 22; Length 312;	
Best Local Similarity	100.0%; Pred. No. 3,6e+58;	
Matches 134; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Qy	48 TTTTATTACTATATGACCAATTTGGCGTCAGAACACACAACTGTGACGAAGGCCCTCCA	107
Db	CCC	160
Qy	1 TTATATATCATATGACCAATTTGGCGTCAGAACACACAACTGTGACGAAGGCCCTCCA	60
Dy	108 AGCCAGAGTTGATCTGAGAACTTCTACTATGTGCATCTTGTAATCCTGATGATGG	167
Qy	61 AGCCAGAGTTGATCTGAGAACTTCTACTATGTGCATCTTGTAATCCTGATGATGG	120
Qy	168 AATGTTCTCTTTCA	181
Dy	121 AATGTTCTCTTTCA	134
RESULT 35		
AAL122773		
ID	AAL122773 standard; DNA; 312 BP.	
AC	AAL122773;	
XT	12-OCT-2001 (first entry)	
DE	Probe #12706 for gene expression analysis in human cervical cell sample.	
KM	Probe; human; microarray; gene expression; cervical epithelial cell;	
KW	cervical cancer; ss.	
OS	Homo sapiens.	
WO	WO200157278-A2.	
PD	09-AUG-2001.	
FF	30-JAN-2001; 2001NO-US00670.	
PR	04-FEB-2000; 2000US-0180112.	
PR	16-MAR-2000; 2000US-0080116.	
PR	30-JUN-2000; 2000US-060840.	
PR	03-AUG-2000; 2000US-0632366.	
PR	21-SEP-2000; 2000US-0234687.	
PR	27-SEP-2000; 2000US-0236359.	
PR	04-OCT-2000; 2000GB-0024263.	
XX	(MOLE-) MOLECULAR DYNAMICS INC.	
XX	Penn SG,	Hanzel DK, Chen W, Rank DR;
XX		


```
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC hyperplasia.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other:
XX
Query Match 74.0%; Score 134; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 TTTTATTACTTATATGCAATTTGGCCGACACACAGCTGACGAGAGGCGCTTCA 107
DB 1 TTTTATTACTTATATGCAATTTGGCCGACACACAGCTGACGAGAGGCGCTTCA 60
QY 108 AGCCAAAGTTGATGCTGAGACTTCTTACTTGTCTGCTGATGCTGATGTTGG 167
DB 61 AGCCAAAGTTGATGCTGAGACTTCTTACTTGTCTGCTGATGCTGATGTTGG 120
QY 168 AATGTTCTCTTCA 181
DB 121 AATGTTCTCTTCA 134
RESULT 38
ABSI6039
ID ABSI6039 standard; DNA; 312 BP.
AC ABSI6039;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe ORF from lung SEQ ID No 16030.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease; open reading frame: ORF.
XX
XX Homo sapiens.
XX
XX W0200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
XX 16-MAR-2000; 2000US-200368P.
XX 03-AUG-2000; 2000US-063236P.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
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XX
XX Claim 4; SEQ ID No 16030; 634bp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes, derived from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX nucleic acid expressed in the human lung; measuring gene expression to a
XX sample derived from human lung, comprising (a) contacting the array with
XX mRNA and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray assigning exons in a genome to the
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORFs) of the probes, or particularly
XX using human lung derived mRNA and for the study of lung diseases
XX such as asthma, lung cancer, chronic obstructive pulmonary disease
XX (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
XX fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
XX Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
XX haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
XX pulmonary alveolar proteinosis, fibrocystic pulmonary dysplasia,
XX and hyaline membrane disease. The present sequence is a single exon
XX probe open reading frame of the invention.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other:
XX
Query Match 74.0%; Score 134; DB 24; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 TTTTATTACTTATATGCAATTTGGCCGACACACAGCTGACGAGAGGCGCTTCA 107
DB 1 TTTTATTACTTATATGCAATTTGGCCGACACACAGCTGACGAGAGGCGCTTCA 60
QY 108 AGCCAAAGTTGATGCTGAGACTTCTTACTTGTCTGCTGATGCTGATGTTGG 167
DB 61 AGCCAAAGTTGATGCTGAGACTTCTTACTTGTCTGCTGATGCTGATGTTGG 120
QY 168 AATGTTCTCTTCA 181
DB 121 AATGTTCTCTTCA 134
RESULT 39
ABN29241
ID ABN29241 standard; DNA; 65 BP.
AC ABN29241;
XX
XX 15-JUL-2002 (first entry)
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:1989.
XX
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Human, mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
 Rattus norvegicus.
 WO200210449-A2.
 07-FEB-2002.
 20-JUL-2001; 2001WO-IB01903.
 28-JUL-2000; 2000US-221607P.
 02-MAY-2001; 2001US-287724P.
 (COMP-) COMPUGEN INC.
 Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S; WPI; 2002-257383/30.
 New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
 Example 1; SEQ ID 1989; 47pp; English.
 The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of a genome. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of specific transcripts in a given tissue. The libraries are only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. The sequence data for this patent did not form part of the printed specification, but is available in electronic format directly from Wipo at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 Sequence 65 BP; 11 A; 18 C; 15 G; 21 T; 0 other;
 Query Match 14.4%; Score 26; DB 24; Length 65;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 139 GTCATCTCTGACCTCATGTGATGAT 164
 DB 13 GTCATCTCTGACCTCATGTGATGAT 38
 RESULT 40
 AS00246
 ID AS00246 standard; DNA; 372 BP.
 AC AAS00246;
 10-MAY-2001 (first entry)
 Rat potassium channel regulatory protein, Mink2, DNA sequence.

Rat; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds; angina; asthma; diabetes; renal insufficiency; urinary incontinence; irritable colon; epilepsy; cerebrovascular ischemia, autoimmune disease.
 Rattus sp.
 Key 1.372
 CDS /*tag= a
 /product= "MINK2 potassium channel protein"
 WO200114403-A1.
 01-MAR-2001.
 18-AUG-2000; 2000MO-US2799.
 20-AUG-1999; 99US-0379201.
 (UYCA-) UNIV CASE WESTERN RESERVE.
 Ficker E, Wible B, Brown AM; WPI; 2001-218424/22.
 P-FSD6; AAS00216.
 Novel potassium channel gene termed Mink2 encoding potassium channel regulatory protein, useful for screening compounds that are useful for treating diseases caused by aberrant potassium activity -
 Claim 1; Fig 10; 39pp; English.
 The sequence represents the coding sequence of rat potassium channel regulatory protein, Mink2, which is useful for screening compounds that are useful for treating diseases caused by aberrant potassium activity, such as human cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal insufficiency, urinary incontinence, irritable colon, epilepsy, cerebrovascular ischemia, and autoimmune disease.
 Sequence 372 BP; 95 A; 98 C; 105 G; 74 T; 0 other;
 Query Match 14.4%; Score 26; DB 22; Length 372;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 139 GTCATCTCTGACCTCATGTGATGAT 164
 DB 145 GTCATCTCTGACCTCATGTGATGAT 170
 RESULT 41
 AAC64072
 ID AAC64072 standard; cDNA; 468 BP.
 AC AAC64072;
 19-FEB-2001 (first entry)
 Rat potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:3.
 Rat; KCNE2; MiRP1; potassium channel protein; KCNE1-related; Mink-related; long QT syndrome; cardiac arrhythmia; drug screening; knockout mouse; transgenic animal; ion channel disorder; KCNE2 delayed rectifier potassium channel; anti-KCNE2 antibody; HERG, 98.
 Rattus norvegicus.
 WO200063434-A1.
 26-OCT-2000.

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XX PF 14-APR-2000; 2000MO-US10004.
XX PR
XX PA
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX PI WPI; 2000-672747/65.
XX DR
XX DR Novel nucleic acids encoding MIRP1, MIRP2 and MIRP3, useful for
XX DR P-PSDS; AAB29586.
XX PT diagnosing and treating ion channel disorders, especially long QT
XX PT syndrome.
XX PT
XX PS Claim 1; Page 119-120; 132pp; English.
XX CC
XX CC The invention relates to novel ion channel proteins related to
XX CC KCNE1 (Mink) and to nucleic acids encoding them. The proteins of
XX CC KCNE1 and KCNE2 (MIRP1; AAB29585 and AAB29586,
XX CC respectively); human and mouse KCNE2 (MIRP2; AAB29587 and AAB29590,
XX CC respectively); human and mouse KCNE4 (MIRP3; AAB29588 and AAB29590,
XX CC respectively). The cDNAs encoding these proteins are given in AAC64071-
XX CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
XX CC potassium channels (I-KR), mutations in which are associated with long QT
XX CC syndrome. The invention also relates to methods of diagnosing long QT
XX CC syndrome using the KCNE2, KCNE3, KCNE4 and KCNE5 genes, a transgenic
XX CC nonhuman animals comprising a heterologous ion channel protein gene
XX CC of the invention, a transgenic animal comprising human KCNE2 and HERG
XX CC DNA, and methods of and screening drugs for treating long QT syndrome
XX CC using KCNE2 proteins (including mutants), nucleic acids encoding them
XX CC and antibodies against KCNE2 proteins. The methods, antibodies, nucleic
XX CC acids, and proteins may be used for diagnosing or treating ion channel
XX CC disorders, especially long QT syndrome. Transgenic animals comprising
XX CC KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
XX CC The present sequence represents cDNA encoding rat KCNE2 (MIRP1).
XX SQ
XX
XX Query Match 14.4%; Score 26; DB 21; Length 468;
XX Best Local Similarity 100.0%; Pred. No. 0.0021;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 139 GTCATCTCTGTACCTCATCGTGATGAT 164
XX
XX DB 179 GTCATCTCTGTACCTCATCGTGATGAT 204
XX
XX RESULT 42
XX AAC64079
XX ID AAC64079 standard; DNA; 23 BP.
XX AC
XX AC AAC64079;
XX DT
XX DT 19-FEB-2001 (first entry)
XX DE
XX DE PCR primer SEQ ID NO:15, used in KCNE2/3/4 SSCP analysis.
XX KW KCNE2; MIRP1; KCNE3; MIRP2; KCNE4; MIRP3; ion channel protein;
XX KW KCNE1-related; Mink-related; long QT syndrome; cardiac arrhythmia;
XX KW drug screening; knockout mouse; transgenic animal; SSCP analysis;
XX KW PCR primer; ss.
XX OS
XX OS Unidentified.
XX RN
XX RN WO200063434-A1.
XX PN
XX PN 26-OCT-2000.
XX PD
XX PD 14-APR-2000; 2000MO-US10004.
XX PF

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XX PR 15-APR-1999; 99US-0129404.
XX PR (UTAH ) UNIV UTAH RES FOUND.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX PI WPI; 2000-672747/65.
XX DR
XX DR Novel nucleic acids encoding MIRP1, MIRP2 and MIRP3, useful for
XX DR diagnosing and treating ion channel disorders, especially long QT
XX DR syndrome.
XX PT Example 1; Page 62; 132pp; English.
XX CC
XX CC The invention relates to novel ion channel proteins related to
XX CC KCNE1 (Mink) and to nucleic acids encoding them. The proteins of
XX CC KCNE1 and KCNE2 (MIRP1; AAB29585 and AAB29586,
XX CC respectively); human and mouse KCNE2 (MIRP2; AAB29587 and AAB29590,
XX CC respectively); human and mouse KCNE4 (MIRP3; AAB29588 and AAB29590,
XX CC respectively). The cDNAs encoding these proteins are given in AAC64071-
XX CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
XX CC potassium channels (I-KR), mutations in which are associated with long QT
XX CC syndrome. The invention also relates to methods of diagnosing long QT
XX CC syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
XX CC disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
XX CC nonhuman animals comprising a heterologous ion channel protein gene
XX CC of the invention, a transgenic animal comprising human KCNE2 and HERG
XX CC DNA, and methods of and screening drugs for treating long QT syndrome
XX CC using KCNE2 proteins (including mutants), nucleic acids encoding them
XX CC and antibodies against KCNE2 proteins. The methods, antibodies, nucleic
XX CC acids, and proteins may be used for diagnosing or treating ion channel
XX CC disorders, especially long QT syndrome. Transgenic animals comprising
XX CC KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
XX CC The present sequence represents cDNA encoding rat KCNE2 (MIRP1).
XX CC The present sequence represents cDNA encoding rat KCNE2 (MIRP1).
XX SQ
XX
XX Query Match 12.7%; Score 23; DB 21; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 0.065;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 34 GTCTTCGAGGATTTTATTAC 56
XX
XX DB 1 GTCTTCGAGGATTTTATTAC 23
XX
XX RESULT 43
XX AAC64078/5
XX ID AAC64078 standard; DNA; 21 BP.
XX AC
XX AC AAC64078;
XX DT
XX DT 19-FEB-2001 (first entry)
XX DE
XX DE PCR primer SEQ ID NO:14, used in KCNE2/3/4 SSCP analysis.
XX KW KCNE2; MIRP1; KCNE3; MIRP2; KCNE4; MIRP3; ion channel protein;
XX KW KCNE1-related; Mink-related; long QT syndrome; cardiac arrhythmia;
XX KW drug screening; knockout mouse; transgenic animal; SSCP analysis;
XX KW PCR primer; ss.
XX OS
XX OS Unidentified.
XX RN
XX RN WO200063434-A1.
XX PN
XX PN 26-OCT-2000.
XX PD
XX PD 14-APR-2000; 2000MO-US10004.
XX PF
XX PF 15-APR-1999; 99US-0129404.

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XX (UTAH) UNIV UTAH RES FOUND.
 PA (UYA) UNIV YALE.
 XX Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
 PI WPI; 2000-67247/65.
 XX Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
 PT diagnosing and treating ion channel disorders, especially long QT
 PT syndrome -
 XX Example 1; Page 62; 132pp; English.
 XX The invention relates to novel ion channel proteins related to
 CC KCHN1 (Mink) and to nucleic acids encoding them. The proteins of
 CC KCHN1 are associated with a cardiac arrhythmia, especially long QT
 CC syndrome, in human and mouse KCHN3 (MiRP2), AAB29586,
 CC respectively; and human and mouse KCHN4 (MiRP3), AAB29589,
 CC respectively; and human and mouse KCHN5 (MiRP4), AAB29590,
 CC respectively). The cDNAs encoding these proteins are given in AAC64071-
 CC AAC64076. KCHN2, along with HERG, forms cardiac fast delayed rectifier
 CC potassium channels (I-Kr), mutations in which are associated with long
 CC QT syndrome. The invention also relates to methods of diagnosing long QT
 CC syndrome using the KCHN2, KCHN3 or KCHN4 genes, a knockout mouse with a
 CC nonhuman animal comprising a heterologous KCHN2 gene, transgenic
 CC nonhuman animal comprising a heterologous KCHN3 gene, and a method
 CC of the invention, a transgenic animal comprising human KCHN2 and HERG
 CC DNA, and methods of and screening drugs for treating long QT syndrome
 CC using KCHN2 proteins (including mutants), nucleic acids encoding them
 CC and antibodies against KCHN2 proteins). The methods, antibodies, nucleic
 CC acids, and proteins may be used for diagnosing or treating ion channel
 CC disorders, especially long QT syndrome. Transgenic animals comprising
 CC KCHN2, HERG, and a heterologous KCHN2 gene, and KCHN2, HERG, and a
 CC KCHN3 gene are also provided. The present invention also provides a method
 CC of the invention, a transgenic animal comprising human KCHN2 and HERG
 CC DNA, and methods of and screening drugs for treating long QT syndrome.
 XX The present sequence represents a PCR primer used to amplify KCHN2.
 XX KCHN3 and KCHN4 gene fragments for SSCP analysis.
 XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;
 XX
 Query Match 11.6%; Score 21; DB 21; Length 21;
 Best-Local Similarity 100.0%; Pred. NO. 0.67; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 QY 103 CTCGACGCAAGTTGATGCT 123
 Db 21 CTCGACGCAAGTTGATGCT 1
 RESULT 44
 AAD35176
 ID AAD35176 standard; DNA; 21 BP.
 AC AAD35176;
 XX 25-JUL-2002 (first entry)
 DT Human KCHN2 gene amplifying forward PCR primer #2.
 XX Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
 KW KCHN2; long QT syndrome; LQTS; cardiac arrhythmia; PCR; primer; ss.
 XX Homo sapiens.
 OS WO200222875-A2.
 XX 21-MAR-2002.
 PD 11-SEP-2001; 2001WO-US28332.
 XX 11-SEP-2000; 2000US-231571P.
 XX (UYA) UNIV YALE.
 PA Goldstein SAN;
 PI

XX WPI; 2002-362360/39.
 XX Novel gene encoding Min-K related ion channel protein subunit and
 PT polymorphisms in this gene associated with antibiotic-induced long QT
 PT syndrome -
 XX Example 1; Page 22; 49pp; English.
 XX The present invention relates to novel KCHN2 genes encoding Min-K related
 CC (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
 CC associated with ion channel disorders including antibiotic-induced long
 CC QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
 CC 57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
 CC encoding the amino acid positions is useful for diagnosing the presence
 CC of a polymorphism that causes drug-induced LQTS. The diagnostic methods
 CC are useful in the development of new drug therapies which selectively
 CC avoid or reduce the risk of drug-induced LQTS. The present invention also
 CC arrhythmias. The present sequence is human KCHN2 gene amplifying PCR
 XX primer. This sequence is used in the exemplification of the invention.
 XX Sequence 21 BP; 4 A; 7 C; 2 G; 8 T; 0 other;
 XX
 Query Match 11.6%; Score 21; DB 24; Length 21;
 Best-Local Similarity 100.0%; Pred. NO. 0.67; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 QY 133 TACTATGTCATCTGTACTCT 153
 Db 1 TACTATGTCATCTGTACTCT 21
 RESULT 45
 AAF80272
 ID AAF80272 standard; DNA; 20 BP.
 AC AAF80272;
 XX 29-JUN-2001 (first entry)
 DT Primer used to amplify potassium channel subunit Isk2 cDNA fragment.
 XX Human; potassium channel; Isk2; gene therapy; gastric motility;
 KW gastric acid secretion; anti-arrhythmic agent; myocardial infarction;
 XX PCR primer; ss.
 XX Homo sapiens.
 OS WO200127246-A1.
 XX 19-APR-2001.
 PD 10-OCT-2000; 2000WO-US28014.
 XX 12-OCT-1999; 99US-0159781.
 XX (MERI) MERCK & CO INC.
 XX Swanson RJ, Liu Y, Folander K;
 PI WPI; 2001-273764/28.
 XX New DNA encoding the Isk2 potassium channel subunit, useful e.g. for
 PT detecting mutations and screening for therapeutic agents -
 XX Example 2; Page 31; 46pp; English.
 XX PCR primers AAF80272-73 were used to amplify a cDNA fragment encoding a
 CC potassium channel subunit, designated Isk2. The Isk2 polynucleotide,
 CC and derived probes, are used diagnostically to detect mutations in the
 CC Isk2 gene, to determine levels of mRNA expression and to isolate
 CC homologous sequences; for recombinant expression of Isk2; in gene
 CC therapy to increase potassium channel activity and to generate

CC transgenic animals, as models and for drug screening. Recombinant IsK2
 CC is used for studying biochemical activity of IsK2 and its role in
 CC disorders of gastric motility and gastric acid secretion, and to raise
 CC specific antibodies. IsK2 modulators are potentially useful for
 CC treating diseases associated with increased or reduced potassium
 CC channel activity, e.g. as anti-arrhythmic agents for treating
 CC myocardial infarction and as regulators of gastric acid secretion.

XX
 SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

Query Match 11.0%; Score 20; DB 22; Length 20;
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 CCTCATGCTGATGATTGGAA 169

Db 1 CCTCATGCTGATGATTGGAA 20

Search completed: June 9, 2003, 12:12:24
 Job time : 184 secs

GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: June 9, 2003, 12:33:26 Search time 82 seconds

(Without alignments)
3089.223 Million cell updates/sec

Title: US-09-550-163-1_COPY_80_260

Perfect score: 181

Sequence: 1 acttaccacattccacac.....gattggaatgtctttcca 181

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 870385 seqs, 69976693 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	181	100.0	372	10	US-09-864-761-33139	Sequence 33139, A
2	181	100.0	450	10	US-09-864-761-3463	Sequence 3463, A
3	181	100.0	712	9	US-10-009-1515-5	Sequence 1515, A
4	181	100.0	712	9	US-10-009-1515-5	Sequence 1515, A
5	181	100.0	113604	9	US-10-227-195A-1	Sequence 1, Appli
6	181	100.0	113604	9	US-10-227-195A-2	Sequence 2, Appli
7	134	74.0	312	10	US-09-864-761-20233	Sequence 20233, A
8	18	9.9	714	10	US-09-864-761-10563	Sequence 10563, A
9	18	9.9	782	10	US-09-772-1348-89	Sequence 89, Appli
10	17	9.4	374	10	US-09-867-701-7019	Sequence 7019, A
11	17	9.4	475	9	US-09-817-921-0222	Sequence 7022, A
12	17	9.4	475	9	US-09-817-921-0222	Sequence 7022, A
13	17	9.4	491	9	US-09-818-995-1925	Sequence 1925, A
14	17	9.4	2197	10	US-09-778-171-1	Sequence 1, Appli
15	17	9.4	32189	9	US-09-764-891-7358	Sequence 7358, A
16	17	9.4	75899	10	US-09-854-883-243	Sequence 243, Appl
17	17	9.4	465237	10	US-09-933-267A-1	Sequence 1, Appli
18	17	9.4	1691139	9	US-10-067-514-1	Sequence 1, Appli
19	16	8.8	334	10	US-09-960-352-12908	Sequence 12908, A

20	16	8.8	438	10	US-09-983-965-3960	Sequence 3960, Ap
21	16	8.8	1842	10	US-09-976-336-1502	Sequence 3361, App
22	16	8.8	1842	10	US-09-976-336-1502	Sequence 3361, App
23	16	8.8	2244	10	US-09-954-455-1174	Sequence 1174, Ap
24	16	8.8	2244	10	US-09-954-455-1174	Sequence 1174, Ap
25	16	8.8	2880	10	US-09-925-301-415	Sequence 415, App
26	16	8.8	2880	10	US-09-925-301-415	Sequence 415, App
27	16	8.8	6047	10	US-09-954-455-498	Sequence 498, App
28	16	8.8	11390	10	US-09-962-700-569	Sequence 569, App
29	16	8.8	11390	10	US-09-962-700-569	Sequence 569, App
30	16	8.8	14796	10	US-09-954-455-173	Sequence 371, App
31	16	8.8	14796	10	US-09-954-455-173	Sequence 371, App
32	16	8.8	14796	10	US-09-910-186A-3	Sequence 3, Appli
33	16	8.8	14796	10	US-09-910-186A-3	Sequence 3, Appli
34	16	8.8	13134	10	US-09-880-107-3421	Sequence 3421, Ap
35	16	8.8	13134	10	US-09-880-107-3421	Sequence 3421, Ap
36	16	8.8	123192	9	US-10-175-523-71	Sequence 71, Appli
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42	15	8.3	81	10	US-09-864-761-23326	Sequence 326, App
43	15	8.3	133	10	US-09-560-863-157	Sequence 157, App
44	15	8.3	133	10	US-09-560-863-157	Sequence 157, App
45	15	8.3	136	10	US-09-770-696-583	Sequence 583, App
46	15	8.3	136	10	US-09-770-696-583	Sequence 583, App
47	15	8.3	271	10	US-09-991-936-464	Sequence 464, App
48	15	8.3	271	10	US-09-991-936-464	Sequence 464, App
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54	15	8.3	274	10	US-09-864-761-19238	Sequence 1938, A
55	15	8.3	280	10	US-09-783-590-2236	Sequence 2236, A
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57	15	8.3	285	10	US-09-924-035A-336	Sequence 336, App
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73	15	8.3	451	9	US-09-918-995-33140	Sequence 33140, A
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75	15	8.3	453	9	US-09-918-995-3384	Sequence 3384, Ap
76	15	8.3	453	9	US-09-764-891-9995	Sequence 9995, Ap
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78	15	8.3	453	9	US-09-864-761-12303	Sequence 12303, Ap
79	15	8.3	453	9	US-09-864-761-12303	Sequence 12303, Ap
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87	15	8.3	501	10	US-09-783-590-4657	Sequence 4657, Ap
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89	15	8.3	516	9	US-09-864-761-8318	Sequence 8318, Ap
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107	15	8.3	868	9	US-10-139-846-1685	Sequence 1685, Ap
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109	15	8.3	871	9	US-10-139-846-1728	Sequence 1728, Ap
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113	15	8.3	896	9	US-10-139-846-997	Sequence 997, App
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115	15	8.3	1135	9	US-09-822-846-16	Sequence 16, Appli
116	15	8.3	1135	9	US-09-822-846-16	Sequence 16, Appli
117	15	8.3	1225	9	US-09-822-846-198	Sequence 198, App
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128	15	8.3	1500	10	US-09-924-501-9	Sequence 9, Appli
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	106	15	8.3	7231	9	US-10-439-676-123	Sequence 123, Ap	c 179	14	7.7	367	9	US-09-878-571-328	Sequence 1638, A
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	110	15	8.3	7960	9	US-09-847-101B-30	Sequence 30, Appl	c 183	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
	111	15	8.3	7960	9	US-09-847-101B-30	Sequence 30, Appl	c 184	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
	112	15	8.3	8883	9	US-09-847-101B-30	Sequence 30, Appl	c 185	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
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	118	15	8.3	14176	10	US-09-764-881-8501	Sequence 8501, Ap	c 191	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
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	130	15	8.3	37474	9	US-09-952-060-25	Sequence 25, Appl	c 203	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
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	134	15	8.3	132762	9	US-09-954-596-17	Sequence 17, Appl	c 207	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
	135	15	8.3	132762	9	US-09-954-596-17	Sequence 17, Appl	c 208	14	7.7	372	10	US-09-918-995-19075	Sequence 19075, A
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 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
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 Sequence No. US0200048763A1
 GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
 APPLICANT: Hada, David A.
 APPLICANT: Hada, David A.
 APPLICANT: Chen, Wenheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Acomica-X-1
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 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
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US-09-864-761-20233

Query Match
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; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Robert
; APPLICANT: Aglate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF OVARIAN CANCER
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10563
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10563

Query Match
Best Local Similarity 100.0%; Pred. No. 5.1; Length 714;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TTACACAGACGCGCTGAA 30
Db 84 TTACACAGACGCGCTGAA 101

RESULT 9
US-09-772-1348-89/c
; Sequence: 89 Application US/097721348
; Patent No. US2002044310A1
; GENERAL INFORMATION:
; APPLICANT: Southern Illinois University
; APPLICANT: Lightfoot, David
; APPLICANT: Meksem, Khalid
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UNDER
; RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH SY
; FILE REFERENCE: 2268/422
; CURRENT APPLICATION NUMBER: US/09/772,1348
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/176,811
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 782
; TYPE: DNA
; ORGANISM: soybean
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(782)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
US-09-772-1348-89

Query Match
Best Local Similarity 100.0%; Pred. No. 5.2; Length 782;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AAGGATTTTATTACTTA 59
Db 781 AAGGATTTTATTACTTA 764

RESULT 10
US-09-867-701-7019
; Sequence 7019, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
```

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; APPLICANT: Jones, Robert
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; PRIORITY FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 1091
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7019
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-7019

Query Match          9.4%; Score 17; DB 10; Length 374;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 CTCGAAGCCAAAGTTGCA 119
Db 122 CTCGAAGCCAAAGTTGCA 138

RESULT 11
US-09-867-701-7022
; Sequence 7022, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Robert A.
; APPLICANT: Jones, Robert A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; PRIORITY FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7022
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-7022

Query Match          9.4%; Score 17; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 CTCGAAGCCAAAGTTGCA 119
Db 122 CTCGAAGCCAAAGTTGCA 138

RESULT 12
US-09-918-995-69
; Sequence 69, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIORITY FILING DATE: 2001-07-30
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-69

Query Match          9.4%; Score 17; DB 9; Length 475;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 GAGCAAGAGGCGCTTCCA 107
Db 204 GAGCAAGAGGCGCTTCCA 220

RESULT 13
US-09-918-995-1925
; Sequence 1925, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIORITY FILING DATE: 2001-07-30
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1925
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-1925

Query Match          9.4%; Score 17; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 GAGCAAGAGGCGCTTCCA 107
Db 168 GAGCAAGAGGCGCTTCCA 184

RESULT 14
US-09-778-171-1/c
; Sequence 1, Application US/09778171
; Patent No. US2002012984A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, et al
; TITLE OF INVENTION: KAWALJIAN SPHINGOSINE-1-PHOSPHATE
; FILE REFERENCE: 20568
; CURRENT APPLICATION NUMBER: US/09/778,171
; PRIORITY FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/180,534
; PRIORITY FILING DATE: 2000-02-07
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2197
; TYPE: DNA
; ORGANISM: Mouse
US-09-778-171-1

Query Match          9.4%; Score 17; DB 10; Length 2197;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 15 CACACGAGCGTGGAG 31
Db 248 CACACGAGCGTGGAG 232

RESULT 15
US-09-764-891-7358
; FILE REFERENCE: US/09764891
; PUBLICATION NO.: US2003007700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/604076
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7358
; LENGTH: 32189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7358

Query Match 9.4%; Score 17; DB 9; Length 32189;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 GTTGATGCTGAGACTT 131
Db 6846 GTTGATGCTGAGACTT 6862

RESULT 16
US-09-854-883-243/c
; Sequence 243, Application US/09854883
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowert
; APPLICANT: Susan M. Preller
; APPLICANT: Brett P. Monis
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; PRIOR APPLICATION NUMBER: US/09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 243
; LENGTH: 5899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-854-883-243

Query Match 9.4%; Score 17; DB 10; Length 75899;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AAGAGTTTATTACTT 58
Db 6963 AAGAGTTTATTACTT 6947

RESULT 17
US-09-933-267A-1
; Sequence 1, Application US/09933267A
; GENERAL INFORMATION:
; APPLICANT: Francis et al.
; TITLE OF INVENTION: Estrogen receptor alpha variants and
; FILE REFERENCE: CLO00258C14
; CURRENT APPLICATION NUMBER: US/09/933,267A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/160626
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 60/183756
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/692414
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/768184
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 09/804076
; PRIOR APPLICATION NUMBER: 09/826314
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 465237
; TYPE: DNA
; ORGANISM: human
US-09-933-267A-1

Query Match 9.4%; Score 17; DB 10; Length 465237;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 ATTATTTACTTAT 62
Db 389257 ATTATTTACTTAT 389273

RESULT 18
US-10-067-514-1/c
; Sequence 1, Application US/10067514
; PUBLICATION NO.: US2003005453A1
; GENERAL INFORMATION:
; APPLICANT: Gretaedottir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; CURRENT FILING DATE: 2002-05-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1

Query Match 9.4%; Score 17; DB 9; Length 1691139;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GAAGAGTTTATTACT 57
Db 690407 GAAGAGTTTATTACT 690391

RESULT 19
US-09-960-352-12908/c
; Sequence 12908, Application US/09960352
; PUBLICATION NO.: US2002037139A1
; GENERAL INFORMATION:

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; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Nishikawa, Yoshitaka
; APPLICANT: Nishikawa, Yoshitaka
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879,536
; PRIOR FILING DATE: 2001-09-21
; PRIOR FILING DATE: 1998-06-10
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 381
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; LOCATOR: (1)-622
; OTHER INFORMATION: n = A,T,C or G
; US-09-879-536-381

Query Match      8.8%; Score 16; DB 10; Length 324;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GATTTTTATTACTTAT 60
DB 316 GATTTTTATTACTTAT 301

RESULT 20
US-09-983-965-2960
; Sequence 2960, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION: Wesley C.
; APPLICANT: Warren, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 2960
; LENGTH 438
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (325),(425)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 20-LI83058-009-Q1-K1-E7
US-09-983-965-2960

Query Match      8.8%; Score 16; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 GACACACACACGCTGAG 93
DB 48 GACACACACACGCTGAG 63

RESULT 21
US-09-879-536-381/C
; Sequence 381, Application US/09879536
; Patent No. US20020144298A1

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; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Nishikawa, Yoshitaka
; APPLICANT: Nishikawa, Yoshitaka
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879,536
; PRIOR FILING DATE: 2001-09-21
; PRIOR FILING DATE: 1998-06-10
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 381
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; LOCATOR: (1)-622
; OTHER INFORMATION: n = A,T,C or G
; US-09-879-536-381

Query Match      8.8%; Score 16; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 TTATATGGACAATTGG 72
DB 22 TTATATGGACAATTGG 7

RESULT 22
US-09-938-842A-1502
; Sequence 1502, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1502
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1502

Query Match      8.8%; Score 16; DB 9; Length 1977;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 AAGTTGATCTGTGAGAA 128

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[illegible]

US-09-851-129A
CURRENT APPLICATION NUMBER: US/09/851,129A
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/165,098
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 16
TYPE: DNA
ORGANISM: Human
US-09-851-129A-16

Query Match 8.8%, Score 16; DB 10; Length 2889;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CCAGACACACACAGCT 90
Db 1128 CCAGACACACACAGCT 1143

RESULT 27
US-09-544-456-498/C
Sequence 498, Application US/09954456
Patent No. US20020115057A1

GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
FILE REFERENCE: 689290-76
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 498
LENGTH: 6047
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-498

Query Match 8.8%, Score 16; DB 10; Length 6047;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CACAGACCTGGGAAGA 32
Db 3355 CACAGACCTGGGAAGA 3340

RESULT 28
US-09-969-708-569
Sequence 569, Application US/09969708
Patent No. US20020102532A1

GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Gene Determination and Therapeutic Screening Using Signat
FILE REFERENCE: 689290-70
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 569
LENGTH: 11990
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-708-569

Query Match 8.8%, Score 16; DB 10; Length 11990;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CCAGACACACACAGCT 90
Db 1390 CCAGACACACACAGCT 1405

RESULT 29
US-10-138-618-35
Sequence 35, Application US/10138618
Publication No. US20030100525A1
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & ROCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/138,618
SEQUENCE NUMBER: 35
FILING DATE: 06-MAY-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/975,080
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-138-618-35
Query Match      8.8%; Score 16; DB 9; Length 14796;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      46 ATTATTATTACTTATA 61
Db      10809 ATTATTATTACTTATA 10824

RESULT 30
US-09-954-456-973
; Sequence 973, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 973
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-973

Query Match      8.8%; Score 16; DB 10; Length 14796;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      46 ATTATTATTACTTATA 61
Db      10809 ATTATTATTACTTATA 10824

RESULT 31
US-09-954-456-1636
; Sequence 1636, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18

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; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1636
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1636

Query Match      8.8%; Score 16; DB 10; Length 14796;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      46 ATTATTATTACTTATA 61
Db      10809 ATTATTATTACTTATA 10824

RESULT 32
US-09-918-186A-3
; Sequence 3, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. I. Frank, Bennett,
; INVENTOR: C. I. Frank, Bennett,
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/99/496,694
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US/98/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US/98/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-186A-3

NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (4518)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-918-186A-3

Query Match      8.8%; Score 16; DB 10; Length 14796;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 46 ATTTTATTACTTATA 61
 Db 10809 ATTTTATTACTTATA 10824

RESULT 33
 US-09-880-107-3421
 ; Sequence 3421, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brockman, Jeffrey
 ; APPLICANT: Evans, David
 ; APPLICANT: Kirschner, Joseph G.
 ; APPLICANT: Kirschner, Joseph G.
 ; APPLICANT: Laeng, Pascal
 ; APPLICANT: Palfreyman, Michael
 ; APPLICANT: Rajan, Prithi
 ; FILE REFERENCE: 3235/1J795-US3
 ; CURRENT APPLICATION NUMBER: US/10/175,523
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/299,151
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/317,828
 ; PRIOR FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/325,150
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US 60/333,047
 ; PRIOR FILING DATE: 2001-10-14
 ; PRIOR APPLICATION NUMBER: US 60/349,936
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/361,834
 ; PRIOR FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 197
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 71
 ; TYPE: DNA
 ; FEATURE: 1429192
 ; ORGANISM: Mus musculus
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U75285
 ; US-09-880-107-3421

Query Match 8.8%; Score 16; DB 10; Length 14796;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 ATTTTATTACTTATA 61
 Db 10809 ATTTTATTACTTATA 10824

RESULT 34
 US-09-764-877-3875/c
 ; Sequence 3875, Application US/09764877
 ; Patent No. US20020147140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; FILE REFERENCE: PC005
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; CURRENT APPLICATION NUMBER: US/09/764,877
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; NUMBER OF SEQ ID NOS: 4031
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 3875
 ; LENGTH: 31314
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: Genbank Accession No. US20020147140A1 U75285
 ; US-09-764-877-3875

Query Match 8.8%; Score 16; DB 10; Length 31314;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AAGGATTTTATTACT 57
 Db 14284 AAGGATTTTATTACT 14269

RESULT 35
 US-10-175-523-71
 ; Sequence 71, Application US/10175523

Publication No. US20030096264A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brockman, Jeffrey
 ; APPLICANT: Evans, David
 ; APPLICANT: Kirschner, Joseph G.
 ; APPLICANT: Kirschner, Joseph G.
 ; APPLICANT: Laeng, Pascal
 ; APPLICANT: Palfreyman, Michael
 ; APPLICANT: Rajan, Prithi
 ; FILE REFERENCE: 3235/1J795-US3
 ; CURRENT APPLICATION NUMBER: US/10/175,523
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/299,151
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/317,828
 ; PRIOR FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/325,150
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US 60/333,047
 ; PRIOR FILING DATE: 2001-10-14
 ; PRIOR APPLICATION NUMBER: US 60/349,936
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/361,834
 ; PRIOR FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 197
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 71
 ; TYPE: DNA
 ; FEATURE: 1429192
 ; ORGANISM: Mus musculus
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U75285
 ; US-10-175-523-71

Query Match 8.8%; Score 16; DB 9; Length 123192;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 GGATTTTATTACTTA 59
 Db 118578 GGATTTTATTACTTA 118593

RESULT 36
 US-09-770-3
 ; Sequence 3, Application US/10185770
 ; Patent No. US20030022217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CECCARO, Toni et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND METHODS OF IDENTIFYING AND USING SUCH MOLECULES
 ; CURRENT APPLICATION NUMBER: US/10/185,770
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIOR FILING DATE: 2001-07-02
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3 186957
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(186957)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-185-770-3

Query Match 8.8%; Score 16; DB 9; Length 186957;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 TACTATATGGCAAT 69

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
 ; OTHER INFORMATION: EST HUMAN HIT: A712346.1, EVALU8 9.70e-01
 ; OTHER INFORMATION: NT HIT: L49349.1, EVALU8 1.60e-01
 ; OTHER INFORMATION: NT HIT: L49349.1, EVALU8 1.60e-01
 ; OTHER INFORMATION: NT HIT: L49349.1, EVALU8 1.60e-01

Query Match 8.3%; Score 15; DB 10; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 GCTGAGCAGAGGCC 102

Db 28 GCTGAGCAGAGGCC 42

RESULT 40
 US-09-560-863-157
 ; Sequence 583, Application US/09560863
 ; Patent No. US20030110803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nehls, Michael C.
 ; APPLICANT: Zambowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: NO. US20020110809A1el Human Polynucleotides and the
 ; APPLICATION: US 00110809A1
 ; FILE REFERENCE: LEX-00110809
 ; CURRENT APPLICATION NUMBER: US/09/560,863
 ; CURRENT FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/132,408
 ; PRIOR FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 1008
 ; SOFTWARE: 15; fastseq for Windows Version 4.0
 ; SEQ ID NO 583
 ; SEQ ID NO 583
 ; LENGTH: 133
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(133)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-560-863-157

Query Match 8.3%; Score 15; DB 10; Length 133;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GATTTTTACTTA 59

Db 88 GATTTTTACTTA 102

RESULT 41
 US-09-770-696-583/c
 ; Sequence 583, Application US/09770696
 ; Patent No. US20010044940A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorlach, Jorn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Janssens, Joshua G.
 ; APPLICANT: Wessner, Jeffrey P.
 ; APPLICANT: Matthews, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Wessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kriker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hoffman, Neil
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; APPLICATION: US 00110809A1
 ; FILE REFERENCE: thaliana
 ; CURRENT APPLICATION NUMBER: US/09/770,696
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,278
 ; PRIOR FILING DATE: 2000-01-27
 ; SOFTWARE: 15; fastseq for Windows Version 4.0
 ; SEQ ID NO 583
 ; SEQ ID NO 583
 ; LENGTH: 136
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-696-583

Query Match 8.3%; Score 15; DB 10; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TTGATGCTGAGACT 130

Db 106 TTGATGCTGAGACT 92

RESULT 42
 US-09-991-936-464/c
 ; Sequence 464, Application US/09991936
 ; Publication No. US20030073827A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brandt, Kevin S.
 ; APPLICANT: Stinebaugh, Dan T.
 ; APPLICANT: Wisniewski, Nancy
 ; TITLE OF INVENTION: FLEA HEAD, NERVE CORO, HINDGUT AND MALPIGHIAN TUBULE
 ; APPLICATION: US 00110809A1
 ; FILE REFERENCE: FC-6-CI
 ; CURRENT APPLICATION NUMBER: US/09/991,936
 ; CURRENT FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: US/09/543,668
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 60/128,704
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 1959
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 464
 ; SEQ ID NO 464
 ; LENGTH: 246
 ; TYPE: DNA
 ; ORGANISM: Ctencephalides felis
 US-09-991-936-464

Query Match 8.3%; Score 15; DB 9; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2.2e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 AAGCCAAAGTTGATG 121

Db 119 AAGCCAAAGTTGATG 105

RESULT 43
 US-09-864-761-20062
 ; Sequence 864, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.

```

APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20662
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION: MAP TO AP000193.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBH100, SIGNAL = 1.3
OTHER INFORMATION: NT HIT: AL163280.2, EVALUE 4.00e-08
OTHER INFORMATION: EST HUMAN HIT: BE222233.1, EVALUE 3.00e-09
OTHER INFORMATION: SWISSPROT HIT: P37246, EVALUE 2.50e-00
US-09-864-761-20062

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Query Match      8.3%; Score 15; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CACACAGCGCTGGA 29
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DB      14 CACACAGCGCTGGA 28

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RESULT 44
US-09-878-574-11763
Sequence 11763 Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 11763
LENGTH: 271
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701064862H1
US-09-878-574-11763

Query Match      8.3%; Score 15; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      108 AGCCAAAGTTGATGC 122
      |||||||||
DB      64 AGCCAAAGTTGATGC 78

RESULT 45
US-09-864-761-19038
Sequence 19038 Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Ranzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30

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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 11:08:01 ; Search time 900 Seconds
(Without alignments)
582.898 Million cell updates/sec

Title: US-09-550-163-1_COPY_80_260

Perfect score: 181

Sequence: 1 atttaccacatttcacaca.....gattggaatgtcttttca 181

Scoring table: Oligo_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2: gb.hg.*

3: gb.in.*

4: gb.in.*

5: gb.ov.*

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9: gb.pr.*

10: gb.ro.*

11: gb.ste.*

12: gb.un.*

13: gb.un.*

14: gb.vi.*

15: en.ba.*

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17: en.hum.*

18: en.in.*

19: en.mus.*

20: en.mus.*

21: en.or.*

22: en.ov.*

23: en.pat.*

24: en.ph.*

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26: en.ro.*

27: en.ste.*

28: en.un.*

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31: en.hg.inv.*

32: en.hg.other.*

33: en.hg.mus.*

34: en.hg.pin.*

35: en.hg.rod.*

36: en.hg.hum.*

37: en.hg.vit.*

38: en.ov.*

39: en.hgo.hum.*

40: en.hgo.mus.*

41: en.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	181	100.0	732	6	AX406940	Sequence
3	181	100.0	732	9	AF071002	Homo sapi
4	181	100.0	702	9	AF071002	Homo sapi
5	181	100.0	24608	9	AF030295	Homo sapi
6	181	100.0	100000	9	AF000320	Homo sapi
7	181	100.0	100000	9	AF000052	Homo sapi
8	181	100.0	100000	9	AF000167	Homo sapi
9	181	100.0	100000	17	AF000120	Homo sapi
10	181	100.0	340000	9	AF001719	Homo sapi
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49	181	100.0	340000	9	AF001719	Homo sapi
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51	181	100.0	340000	9	AF001719	Homo sapi
52	181	100.0	340000	9	AF001719	Homo sapi
53	181	100.0	340000	9	AF001719	Homo sapi
54	181	100.0	340000	9	AF001719	Homo sapi
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58	181	100.0	340000	9	AF001719	Homo sapi
59	181	100.0	340000	9	AF001719	Homo sapi
60	181	100.0	340000	9	AF001719	Homo sapi
61	181	100.0	340000	9	AF001719	Homo sapi
62	181	100.0	340000	9	AF001719	Homo sapi
63	181	100.0	340000	9	AF001719	Homo sapi
64	181	100.0	340000	9	AF001719	Homo sapi
65	181	100.0	340000	9	AF001719	Homo sapi

66	18	9.9	112518	2	AC097147	AC097147 Rattus no	139	17	9.4	3725	9	AF133588
67	18	9.9	114212	2	AL355856	AL355856 Homo sapi	140	17	9.4	3822	9	AF133588
68	18	9.9	116135	2	AC094899	AC094899 Rattus no	141	17	9.4	4016	3	BM6728CP
69	18	9.9	121362	9	AL359203	AL359203 Human DNA	142	17	9.4	4056	14	AF389453
70	18	9.9	122113	9	AC095071	AC095071 Homo sapi	143	17	9.4	4056	9	AF389453
71	18	9.9	122113	9	AC095071	AC095071 Homo sapi	144	17	9.4	4056	9	AF389453
72	18	9.9	135650	9	AL583854	AL583854 Human DNA	145	17	9.4	8530	6	AC146557
73	18	9.9	137955	2	AC109290	AC109290 Mus muscu	146	17	9.4	9001	9	AC090020
74	18	9.9	139629	2	AP003809	AP003809 Oryza sat	147	17	9.4	23286	1	BACPNAYPP
75	18	9.9	140533	9	AC097958	AC097958 Homo sapi	148	17	9.4	31607	2	AC1031378
76	18	9.9	140788	9	HS080924	Z9975758 Human DNA	149	17	9.4	41280	9	AL589906
77	18	9.9	143063	2	AC069936	AC069936 Homo sapi	150	17	9.4	51565	9	AC007745
78	18	9.9	143848	2	AC069936	AC069936 Homo sapi	151	17	9.4	51770	9	AL590490
79	18	9.9	144553	9	AL353156	AL353156 Human DNA	152	17	9.4	57294	2	SC025882
80	18	9.9	146545	2	AC104009	AC104009 Homo sapi	153	17	9.4	62370	2	AL451008
81	18	9.9	151482	9	AC068765	AC068765 Homo sapi	154	17	9.4	62377	2	AL451008
82	18	9.9	156140	9	AC067745	AC067745 Homo sapi	155	17	9.4	64677	2	AC079102
83	18	9.9	161788	2	AC025639	AC025639 Homo sapi	156	17	9.4	64931	10	AF1320600S1
84	18	9.9	161935	2	AC096075	AC096075 Rattus no	157	17	9.4	66668	2	AC119961
85	18	9.9	163315	2	AC026876	AC026876 Homo sapi	158	17	9.4	68589	9	HS23702
86	18	9.9	163315	2	AC026876	AC026876 Homo sapi	159	17	9.4	70332	2	AC122618
87	18	9.9	163315	2	AC026876	AC026876 Homo sapi	160	17	9.4	70332	2	AC122618
88	18	9.9	168661	9	AL354855	AL354855 Human DNA	161	17	9.4	74109	8	NGB11445
89	18	9.9	168794	2	AC026252	AC026252 Homo sapi	162	17	9.4	77531	2	AC185652
90	18	9.9	169733	2	AC068046	AC068046 Homo sapi	163	17	9.4	83676	2	AC129856
91	18	9.9	170343	8	AP005185	AP005185 Oryza sat	164	17	9.4	85910	2	AC098836
92	18	9.9	170371	8	AB026295	AB026295 Oryza sat	165	17	9.4	87172	2	AF1723317_3
93	18	9.9	172859	2	AC024320	AC024320 Homo sapi	166	17	9.4	87705	9	HS063215
94	18	9.9	174015	2	AC136367	AC136367 Rattus no	167	17	9.4	88119	2	AL049821
95	18	9.9	174015	2	AC136367	AC136367 Rattus no	168	17	9.4	88293	9	AL713965
96	18	9.9	176399	9	CN069TE1	AL3559358 Human chr	169	17	9.4	89750	2	AC109412
97	18	9.9	180163	9	AP001925	AP001925 Homo sapi	170	17	9.4	94244	9	AC063938
98	18	9.9	180211	9	CN0505TD2	AL3589222 Human chr	171	17	9.4	95736	2	AC037474
99	18	9.9	180222	2	AC0959224	AC0959224 Rattus no	172	17	9.4	97386	9	AC037453
100	18	9.9	181977	2	AC103487	AC103487 Rattus no	173	17	9.4	97561	2	AC098031
101	18	9.9	184490	9	HS082828	HS082828 Homo sapien	174	17	9.4	98119	9	AC024263
102	18	9.9	186258	2	AC097563	AC097563 Rattus no	175	17	9.4	100810	2	AC094252
103	18	9.9	186258	2	AC097563	AC097563 Rattus no	176	17	9.4	100810	2	AC094252
104	18	9.9	189476	2	AC008983	AC008983 Homo sapi	177	17	9.4	101121	9	AC092919
105	18	9.9	191179	2	AC091476	AC091476 Mus muscu	178	17	9.4	102740	2	AC096785_3
106	18	9.9	203959	9	AP001137	AP001137 Homo sapi	179	17	9.4	104215	2	AC123491
107	18	9.9	212038	2	AC110816	AC110816 Mus muscu	180	17	9.4	104234	9	AC078907
108	18	9.9	213462	10	AC077689	AC077689 Mus Muscu	181	17	9.4	105579	9	AF282885
109	18	9.9	213462	10	AC077689	AC077689 Mus Muscu	182	17	9.4	105579	9	AF282885
110	18	9.9	213462	10	AC077689	AC077689 Mus Muscu	183	17	9.4	105579	9	AF282885
111	18	9.9	213884	9	AC068365	AC068365 Homo sapi	184	17	9.4	110000	2	AC092450_2
112	18	9.9	219151	2	AC115353	AC115353 Rattus no	185	17	9.4	110000	2	AC092450_2
113	18	9.9	219769	10	AC067964	AC067964 Mus Muscu	186	17	9.4	110000	2	AC092450_2
114	18	9.9	225962	2	AC125174	AC125174 Mus Muscu	187	17	9.4	110000	2	AC092450_2
115	18	9.9	225962	14	AF250284	AF250284 Amnacta m	188	17	9.4	111466	2	AC104274
116	18	9.9	229371	2	AC121602	AC121602 Mus muscu	189	17	9.4	112591	8	AC066156
117	18	9.9	234116	10	AL596136	AL596136 Mouse DNA	190	17	9.4	112591	8	AC066156
118	18	9.9	234116	10	AL596136	AL596136 Mouse DNA	191	17	9.4	112591	8	AC066156
119	18	9.9	234116	10	AL596136	AL596136 Mouse DNA	192	17	9.4	112591	8	AC066156
120	18	9.9	340000	9	AP001681	AP001681 Homo sapi	193	17	9.4	113746	2	AC110995
121	18	9.9	343550	1	BS003587	AP003587 Nostoc sp	194	17	9.4	113746	2	AC110995
122	18	9.4	485	1	BS003587	AP003587 Nostoc sp	195	17	9.4	113746	2	AC110995
123	18	9.4	676	9	HS0332056	HS0332056 Homo sapi	196	17	9.4	113746	2	AC110995
124	17	9.4	762	8	AF378035	AF378035 Triticum	197	17	9.4	113746	2	AC110995
125	17	9.4	1290	7	HS0332056	HS0332056 Homo sapi	198	17	9.4	113746	2	AC110995
126	17	9.4	1422	10	AF090953	AF090953 Mus muscu	199	17	9.4	121352	2	AC098871
127	17	9.4	1422	10	AF090953	AF090953 Mus muscu	200	17	9.4	121352	2	AC098871
128	17	9.4	1754	8	AF274864	AF274864 Brachia	201	17	9.4	123830	2	AC100244
129	17	9.4	1859	10	BC009013	BC009013 Mus muscu	202	17	9.4	124028	9	AC0322417
130	17	9.4	2147	10	AF247177	AF247177 Mus muscu	203	17	9.4	125217	8	AC097627
131	17	9.4	2199	10	AB004109	AB004109 Chinese h	204	17	9.4	125217	8	AC097627
132	17	9.4	2384	9	AC023309	AC023309 Homo sapi	205	17	9.4	131231	2	AC108734
133	17	9.4	2693	2	AC030350	AC030350 Arabidops	206	17	9.4	131231	2	AC108734
134	17	9.4	2693	2	AC030350	AC030350 Arabidops	207	17	9.4	131231	2	AC108734
135	17	9.4	2793	8	WEPHD1	D73410 Zea mays mR	208	17	9.4	131766	2	AC120451
136	17	9.4	2804	6	AR005012	AR005012 Sequence	209	17	9.4	132444	9	AC091878
137	17	9.4	3424	8	SC0V07484	AF047484 Vibrio vu	210	17	9.4	132526	2	AC120946
138	17	9.4	3641	8	SC0V07484	AF047484 Vibrio vu	211	17	9.4	133894	2	AC105740

C 212	9.4	134060	9	AL358954	Human DNA	285	17	9.4	168467	9	AL138820	Human DNA
C 213	17	9.4	134133	9	AL102487	Human DNA	286	17	9.4	169413	9	AL138820
C 214	17	9.4	134133	9	AL102487	Human DNA	C 287	17	9.4	169413	9	AL138820
C 215	17	9.4	135055	2	AC011873	Homo sapi	C 288	17	9.4	169794	2	AC004688
C 216	17	9.4	135051	2	AC011873	Homo sapi	C 289	17	9.4	170240	2	AL160279
C 217	17	9.4	136115	2	AC012021	Rattus no	C 290	17	9.4	170283	2	AL160279
C 218	17	9.4	136120	2	AC012021	Rattus no	C 291	17	9.4	170763	2	AC000919
C 219	17	9.4	136120	2	AC012021	Rattus no	C 292	17	9.4	171656	2	AC012467
C 220	17	9.4	136707	2	AL157112	Human DNA	C 293	17	9.4	171656	2	AC012467
C 221	17	9.4	139086	2	AL136127	Human DNA	C 294	17	9.4	172092	2	AC011341
C 222	17	9.4	139993	2	AL128283	Rattus no	C 295	17	9.4	172380	2	AC009533
C 223	17	9.4	140582	2	AL128429	Rattus no	C 296	17	9.4	173317	2	AC016637
C 224	17	9.4	140929	2	AL117805	Mus muscu	C 297	17	9.4	173375	2	AC014815
C 225	17	9.4	142690	2	AC012027	Mus muscu	C 298	17	9.4	173414	2	AC012529
C 226	17	9.4	142979	9	AC000029	Homo sapi	C 299	17	9.4	173712	2	AC009894
C 227	17	9.4	143052	9	AL129887	Human DNA	C 300	17	9.4	174311	2	AC009846
C 228	17	9.4	143515	8	AC003928	Human DNA	C 301	17	9.4	174311	2	AC009846
C 229	17	9.4	144249	2	AC001162	Human DNA	C 302	17	9.4	175142	2	AC006850
C 230	17	9.4	145784	9	AP001836	Homo sapi	C 303	17	9.4	175142	2	AC006850
C 231	17	9.4	146395	2	AC017918	Rattus no	C 304	17	9.4	176291	2	AC004610
C 232	17	9.4	146462	2	AC080142	Mus muscu	C 305	17	9.4	176877	2	AC126293
C 233	17	9.4	146810	9	H8179115A	Human DNA	C 306	17	9.4	176899	2	AC126293
C 234	17	9.4	147085	2	AP005586	Oryza sat	C 307	17	9.4	177028	2	AF192304
C 235	17	9.4	147085	2	AP005586	Oryza sat	C 308	17	9.4	177108	2	AC026504
C 236	17	9.4	148452	2	AL136353	Homo sapi	C 309	17	9.4	177211	2	AP005467
C 237	17	9.4	148452	2	AL136353	Homo sapi	C 310	17	9.4	178023	2	AC010705
C 238	17	9.4	149751	2	AC014833	Homo sapi	C 311	17	9.4	178023	2	AC010705
C 239	17	9.4	149968	2	AC011929	Homo sapi	C 312	17	9.4	178415	2	AC023547
C 240	17	9.4	151006	2	AC107255	Rattus no	C 313	17	9.4	178415	2	AC023547
C 241	17	9.4	151418	9	AL183551	Rattus no	C 314	17	9.4	178857	2	AC113658
C 242	17	9.4	152001	9	AL104569	Homo sapi	C 315	17	9.4	179414	9	AC009698
C 243	17	9.4	152010	9	AC026785	Homo sapi	C 316	17	9.4	180973	9	AC029333
C 244	17	9.4	152427	2	AL109138	Homo sapi	C 317	17	9.4	180973	9	AC029333
C 245	17	9.4	152552	2	AL356105	Homo sapi	C 318	17	9.4	181136	2	AC090611
C 246	17	9.4	152602	2	AC026193	Homo sapi	C 319	17	9.4	181739	2	AC111605
C 247	17	9.4	153361	2	AP001990	Homo sapi	C 320	17	9.4	181837	2	AC092901
C 248	17	9.4	153607	2	AL355523	Homo sapi	C 321	17	9.4	182147	2	AC062032
C 249	17	9.4	153805	9	AC090987	Homo sapi	C 322	17	9.4	182496	2	AC011190
C 250	17	9.4	152580	9	AC024597	Homo sapi	C 323	17	9.4	182496	2	AC011190
C 251	17	9.4	152580	9	AC024597	Homo sapi	C 324	17	9.4	182524	2	AC027527
C 252	17	9.4	155676	2	AC004780	Homo sapi	C 325	17	9.4	182524	2	AC027527
C 253	17	9.4	155724	2	AC024714	Homo sapi	C 326	17	9.4	184748	2	AC127231
C 254	17	9.4	156319	2	AC012038	Mus muscu	C 327	17	9.4	184748	2	AC127231
C 255	17	9.4	157519	8	AP001389	Oryza sat	C 328	17	9.4	184573	9	AC091429
C 256	17	9.4	157861	2	AL356302	Rattus no	C 329	17	9.4	184838	2	AC090740
C 257	17	9.4	158665	2	AL356338	Homo sapi	C 330	17	9.4	185648	2	AC113710
C 258	17	9.4	158703	2	AL159770	Mus muscu	C 331	17	9.4	185758	2	AC105460
C 259	17	9.4	160402	2	AC094402	Mus muscu	C 332	17	9.4	186184	2	AC112562
C 260	17	9.4	160487	2	AC094402	Mus muscu	C 333	17	9.4	186184	2	AC112562
C 261	17	9.4	160779	10	AL7323449	Mouse DNA	C 334	17	9.4	186927	2	AC079844
C 262	17	9.4	160851	2	AL105944	Mus muscu	C 335	17	9.4	187135	2	AC122325
C 263	17	9.4	161417	9	AL356358	Human DNA	C 336	17	9.4	187933	2	AC055822
C 264	17	9.4	161476	2	AC026321	Homo sapi	C 337	17	9.4	188096	2	AC127260
C 265	17	9.4	161675	2	AP001975	Homo sapi	C 338	17	9.4	188224	2	AC102068
C 266	17	9.4	161950	2	AC024723	Homo sapi	C 339	17	9.4	188451	2	AC007528
C 267	17	9.4	162454	2	AC012558	Mus muscu	C 340	17	9.4	189129	2	AC024682
C 268	17	9.4	162454	2	AC012558	Mus muscu	C 341	17	9.4	189129	2	AC024682
C 269	17	9.4	162455	2	AC006084	Rattus no	C 342	17	9.4	189574	2	AC094430
C 270	17	9.4	162793	2	AL124391	Mus muscu	C 343	17	9.4	190444	2	AC098121
C 271	17	9.4	162903	2	AL129144	Rattus no	C 344	17	9.4	190568	2	AC011710
C 272	17	9.4	162925	2	AP004461	Oryza sat	C 345	17	9.4	191866	2	AC068676
C 273	17	9.4	162943	9	AC009043	Homo sapi	C 346	17	9.4	192531	5	AL772193
C 274	17	9.4	163027	9	AC002549	Homo sapi	C 347	17	9.4	192531	5	AL772193
C 275	17	9.4	163027	9	AC002549	Homo sapi	C 348	17	9.4	192531	5	AL772193
C 276	17	9.4	164396	2	AC001568	Homo sapi	C 349	17	9.4	192531	5	AL772193
C 277	17	9.4	164429	2	AC026366	Homo sapi	C 350	17	9.4	193575	2	AC105970
C 278	17	9.4	165016	2	AC005574	Homo sapi	C 351	17	9.4	194057	2	AC116940
C 279	17	9.4	165237	6	AX232505	Sequence	C 352	17	9.4	195229	2	AC124545
C 280	17	9.4	165608	8	AC003492	Homo sapi	C 353	17	9.4	196085	2	AC1016737
C 281	17	9.4	166485	9	AC008707	Homo sapi	C 354	17	9.4	196516	2	AL844218
C 282	17	9.4	167212	2	AL127101	Rattus no	C 355	17	9.4	197550	9	CNS01RHP
C 283	17	9.4	167212	2	AL127101	Rattus no	C 356	17	9.4	197551	9	AL390840
C 284	17	9.4	167459	2	CNS01DMX	Homo sapi	C 357	17	9.4	198433	2	AL130067

358	17	9.4	198306	2	ALB37510	ALB37510 Mus muscu	c 431	16	8.8	683	8	AF394008	Cookeina
359	17	9.4	198422	2	AL113939	AL113939 Mus muscu	c 432	16	8.8	689	8	AF394011	Cookeina
360	17	9.4	198901	2	AC116303	AC116303 Homo sapi	c 433	16	8.8	752	6	AO9290	Human sapi
361	17	9.4	200311	2	AC123769	AC123769 Homo sapi	c 434	16	8.8	758	9	HSN4941865	Human sapi
362	17	9.4	201726	2	AC225552	AC225552 Homo sapi	c 435	16	8.8	780	8	CNS014DFU	Human sapi
363	17	9.4	202161	2	AC225552	AC225552 Homo sapi	c 436	16	8.8	780	8	CNS014DFU	Human sapi
364	17	9.4	202161	2	AC225552	AC225552 Homo sapi	c 437	16	8.8	780	8	CNS014DFU	Human sapi
365	17	9.4	202555	2	AC087276	AC087276 Homo sapi	c 438	16	8.8	930	10	AF282282	Human sapi
366	17	9.4	202765	2	AC005181	AC005181 Homo sapi	c 439	16	8.8	930	10	AF282282	Human sapi
367	17	9.4	202866	2	AC092109	AC092109 Homo sapi	c 440	16	8.8	936	1	AF195465	Human sapi
368	17	9.4	203395	2	AC073596	AC073596 Homo sapi	c 441	16	8.8	1053	3	AF138139	Styphlome
369	17	9.4	203579	2	AL645762	AL645762 Homo sapi	c 442	16	8.8	1074	6	AF221830	Sequence
370	17	9.4	208307	2	AC073351	AC073351 Mus muscu	c 443	16	8.8	1078	3	AF398638	Human sapi
371	17	9.4	208307	2	AC073351	AC073351 Mus muscu	c 444	16	8.8	1078	3	AF398638	Human sapi
372	17	9.4	209632	2	AC121084	AC121084 Mus muscu	c 445	16	8.8	1092	9	AF543926	Human sapi
373	17	9.4	210000	2	AC009527	AC009527 Homo sapi	c 446	16	8.8	1093	9	AB041354	Human sapi
374	17	9.4	210361	2	AL671335	AL671335 Mus muscu	c 447	16	8.8	1093	9	AB041354	Human sapi
375	17	9.4	210672	2	HS179115	HS179115 Homo sapien	c 448	16	8.8	1454	3	AF398641	Styphlod
376	17	9.4	210677	2	AC074305	AC074305 Mus muscu	c 449	16	8.8	1520	9	AF4381206	Human sapi
377	17	9.4	211759	2	AC106937	AC106937 Rattus no	c 450	16	8.8	1520	9	D86227	Homo sapien
378	17	9.4	212638	2	AC106937	AC106937 Rattus no	c 451	16	8.8	1520	9	D86227	Homo sapien
379	17	9.4	212638	2	AC106937	AC106937 Rattus no	c 452	16	8.8	1520	9	D86227	Homo sapien
380	17	9.4	212884	2	AC124443	AC124443 Mus muscu	c 453	16	8.8	1549	9	HSN400602	Human sapi
381	17	9.4	213296	2	AC067784	AC067784 Homo sapi	c 454	16	8.8	1552	14	AB028247	Notwalk-1
382	17	9.4	213308	2	AC098281	AC098281 Rattus no	c 455	16	8.8	1553	6	BD011872	Detection
383	17	9.4	213680	1	BSUB0012	2991515 Bacillus su	c 456	16	8.8	1593	14	AB031013	Notwalk-1
384	17	9.4	214000	10	AC093317	AC093317 Mus muscu	c 457	16	8.8	1593	23	BD004352	Detection
385	17	9.4	215260	2	AC094600	AC094600 Homo sapi	c 458	16	8.8	1598	9	HUMN95X	Human orci
386	17	9.4	215260	2	AC094600	AC094600 Homo sapi	c 459	16	8.8	1598	9	HUMN95X	Human orci
387	17	9.4	216733	10	AL593892	AL593892 Homo sapi	c 460	16	8.8	1698	9	AB062285	Homo sapi
388	17	9.4	216825	2	AC108908	AC108908 Homo sapi	c 461	16	8.8	1711	9	BC000164	Homo sapi
389	17	9.4	217250	2	AC019595	AC019595 Homo sapi	c 462	16	8.8	1711	9	BC000164	Homo sapi
390	17	9.4	217286	10	AC098713	AC098713 Mus muscu	c 463	16	8.8	1750	8	AF087912	Arabidops
391	17	9.4	217290	2	AC074332	AC074332 Mus muscu	c 464	16	8.8	1809	9	AF431970	Homo sapi
392	17	9.4	220546	2	AC124742	AC124742 Mus muscu	c 465	16	8.8	1818	1	AF267223	Candidatu
393	17	9.4	220623	3	AE004351	AE004351 Drosophill	c 466	16	8.8	1837	9	AK056940	Homo sapi
394	17	9.4	220623	3	AE004351	AE004351 Drosophill	c 467	16	8.8	1837	9	AK056940	Homo sapi
395	17	9.4	222337	2	AC121849	AC121849 Mus muscu	c 468	16	8.8	2042	6	BTU7568	Sequence
396	17	9.4	222337	2	AC121849	AC121849 Mus muscu	c 469	16	8.8	2042	6	BTU7568	Sequence
397	17	9.4	224299	2	AC130533	AC130533 Homo sapi	c 470	16	8.8	2053	4	AF285059	Ovis arie
398	17	9.4	224406	2	AC098244	AC098244 Rattus no	c 471	16	8.8	2166	9	BC032942	Homo sapi
399	17	9.4	225518	2	AC126458	AC126458 Mus muscu	c 472	16	8.8	2288	9	AK023335	Homo sapi
400	17	9.4	227028	2	AL089140	AL089140 Mus muscu	c 473	16	8.8	2288	9	AK023335	Homo sapi
401	17	9.4	227028	2	AL089140	AL089140 Mus muscu	c 474	16	8.8	2288	9	AK023335	Homo sapi
402	17	9.4	233965	2	AC123543	AC123543 Mus muscu	c 475	16	8.8	2288	9	AK023335	Homo sapi
403	17	9.4	242918	2	AC127347	AC127347 Mus muscu	c 476	16	8.8	2259	4	AF281677	Bob tauu
404	17	9.4	243179	2	AC123863	AC123863 Homo sapi	c 477	16	8.8	2263	3	LMU29952	Leishmania
405	17	9.4	251124	9	HUAB0006060	AE000660 Homo sapi	c 478	16	8.8	2266	8	AY099873	Arabidops
406	17	9.4	252358	2	AC126686	AC126686 Mus muscu	c 479	16	8.8	2315	5	DGVSU2TRAN	Discopysp
407	17	9.4	257912	2	AC126280	AC126280 Mus muscu	c 480	16	8.8	2316	5	AK14690	HPV-1a DNA
408	17	9.4	263649	2	AC125037	AC125037 Mus muscu	c 481	16	8.8	2371	1	U01165	Calulobacter
409	17	9.4	263649	2	AC125037	AC125037 Mus muscu	c 482	16	8.8	2371	1	U01165	Calulobacter
410	17	9.4	275253	2	AC068772	AC068772 Homo sapi	c 483	16	8.8	2516	14	NOB890JB	Normalv
411	17	9.4	282375	2	AC101820	AC101820 Mus muscu	c 484	16	8.8	2558	3	AY071327	Drosophill
412	17	9.4	296683	2	AC124346	AC124346 Homo sapi	c 485	16	8.8	2684	9	AK055329	Homo sapi
413	17	9.4	301450	1	AP001185	AP001185 Clostridi	c 486	16	8.8	2942	10	HMU250723	Mus muscu
414	17	9.4	306130	2	AC110996	AC110996 Homo sapi	c 487	16	8.8	3284	9	HSDESMIN	Human Gene
415	17	9.4	308676	2	AC068639	AC068639 Homo sapi	c 488	16	8.8	3338	8	AF105912	Hordeum v
416	17	8.8	165	1	AF505929	AF505929 atb1351.17	c 489	16	8.8	3423	3	AT021863	Drosophill
417	17	8.8	165	1	AF505929	AF505929 atb1351.17	c 490	16	8.8	3423	3	AT021863	Drosophill
418	17	8.8	334	11	GI0245	GI0245 human STS	c 491	16	8.8	3492	9	AF136976	Homo sapi
419	17	8.8	343	8	AF529291	AF529291 Cookeina	c 492	16	8.8	3497	9	BC012430	Homo sapi
420	17	8.8	379	11	GS1759	GS1759 SHGC-84529	c 493	16	8.8	3569	10	MU250724	Mus muscu
421	17	8.8	385	13	AF151796	AF151796 Butus ma	c 494	16	8.8	3586	3	DROINSUR	Melanoglas
422	17	8.8	394	11	GP09033	GP09033 human STS	c 495	16	8.8	3605	9	AF016991	Callitric
423	17	8.8	559	8	AF394005	AF394005 Cookeina	c 496	16	8.8	3607	9	AF013813	Callitric
424	17	8.8	559	8	AF394005	AF394005 Cookeina	c 497	16	8.8	3607	9	AF013813	Callitric
425	17	8.8	601	8	AF394013	AF394013 Cookeina	c 498	16	8.8	5293	1	TRU11682	Trypanoplas
426	17	8.8	631	8	AF394013	AF394013 Cookeina	c 499	16	8.8	5293	1	TRU11682	Trypanoplas
427	17	8.8	651	8	AF39361	AF39361 Homo sapi	c 500	16	8.8	5350	9	HS200KDU5	Haplopien
428	17	8.8	656	8	AF394012	AF394012 Cookeina	c 501	16	8.8	5807	6	AK346057	Sequence
429	17	8.8	674	8	AF394007	AF394007 Cookeina	c 502	16	8.8	5962	6	AK346168	Sequence
430	17	8.8	677	8	AF394006	AF394006 Cookeina	c 503	16	8.8	6047	6	AK333016	Sequence

550	16	8	8	912813	9	AC106810	Human sapi	723	16	8	8	116620	2	AC123132	Rattus no
551	16	8	8	92859	9	AC106810	Human sapi	724	16	8	8	116620	2	AC123132	Rattus no
552	16	8	8	93432	9	AC106810	Human sapi	725	16	8	8	116691	9	HSJ570012	Human sapi
553	16	8	8	94019	9	AC1159971	Human DNA	726	16	8	8	116841	2	AP000643	Human sapi
554	16	8	8	95727	9	AC091231	Human sapi	727	16	8	8	117487	2	AP002335	Human sapi
555	16	8	8	95782	9	AC025775	Human sapi	728	16	8	8	118309	2	AP004180	Oryza sat
556	16	8	8	96026	2	AC097756	Rattus no	729	16	8	8	118327	9	AC004521	Human sapi
557	16	8	8	96120	2	AC093169	Human sapi	730	16	8	8	118327	9	AC004521	Human sapi
558	16	8	8	96120	2	AC093169	Human sapi	731	16	8	8	119365	5	AL645782	Zebrafish
559	16	8	8	97165	2	AC056257	Human sapi	732	16	8	8	119617	2	AC129382	Rattus no
560	16	8	8	97710	8	AP004471	Human sapi	733	16	8	8	119617	2	AC129382	Rattus no
561	16	8	8	97860	9	AC091816	Human sapi	734	16	8	8	120662	9	AC105388	Human sapi
562	16	8	8	97970	9	AC105596	Rattus no	735	16	8	8	120990	2	OSJN01011	Oryza sat
563	16	8	8	98146	9	AP002297	Human sapi	736	16	8	8	121080	2	AC120314	Rattus no
564	16	8	8	98856	9	AC113150	Human sapi	737	16	8	8	121958	9	AL583838	Human sapi
565	16	8	8	99013	2	AC123161	Rattus no	738	16	8	8	122118	5	AL592106	Zebrafish
566	16	8	8	99013	2	AC123161	Rattus no	739	16	8	8	122118	5	AL592106	Zebrafish
567	16	8	8	99560	9	AC104637	Human sapi	740	16	8	8	122427	7	AC025459	Human sapi
568	16	8	8	100282	9	AC096298	Rattus no	741	16	8	8	122437	7	AC025459	Human sapi
569	16	8	8	100899	9	AC026436	Human sapi	742	16	8	8	122912	2	AC125783	Oryza sat
570	16	8	8	101149	2	AC118492	Rattus no	743	16	8	8	122948	9	HSB91H21	Human sapi
571	16	8	8	101615	9	AC004038	Human sapi	744	16	8	8	123192	10	AF1213151	Mus muscu
572	16	8	8	102255	2	AC026735	Human sapi	745	16	8	8	123209	9	AT164745	Arabidops
573	16	8	8	102629	9	AC093687	Rattus no	746	16	8	8	123209	9	AT164745	Arabidops
574	16	8	8	102629	9	AC093687	Rattus no	747	16	8	8	123209	9	AT164745	Arabidops
575	16	8	8	102871	5	AC095774	Rattus no	748	16	8	8	124377	2	AP005390	Oryza sat
576	16	8	8	102905	9	AC003423	Human sapi	749	16	8	8	124621	5	AC010314	Human sapi
577	16	8	8	103738	8	ATTB010	Human sapi	750	16	8	8	124925	2	AC096184	Rattus no
578	16	8	8	103787	8	ATTB010	Human sapi	751	16	8	8	125145	2	AC096184	Rattus no
579	16	8	8	104079	9	AC119635	Human sapi	752	16	8	8	125571	2	AP003703	Oryza sat
580	16	8	8	104099	9	AC119635	Human sapi	753	16	8	8	125571	2	AP003703	Oryza sat
581	16	8	8	104193	2	AC11									

C 796	16	8.8	137751	10	AC091452	AC091452 Mus muscu	C 869	16	8.8	148177	9	HS1068E13	AL015563 Human DNA
C 797	16	8.8	132321	9	AC095311	Rattus no	C 870	16	8.8	148206	9	AC133593	AC133593 Rattus no
C 798	16	8.8	138477	2	CNS06C7V	AL711745	C 871	16	8.8	148296	9	AC133593	AC133593 Rattus no
C 799	16	8.8	138733	2	AC114385	Rattus no	C 872	16	8.8	148405	9	AC061971	AC061971 Homo sapi
C 800	16	8.8	138793	2	AC114385	Rattus no	C 873	16	8.8	148438	9	AC019072	AC019072 Homo sapi
C 801	16	8.8	139019	2	AC128044	Rattus no	C 874	16	8.8	148438	9	AC019072	AC019072 Homo sapi
C 802	16	8.8	139019	2	AC128044	Rattus no	C 875	16	8.8	148477	9	AC0190851	AC0190851 Rattus no
C 803	16	8.8	139054	2	AC0166510	Rattus no	C 876	16	8.8	148567	9	CNS01HGK1	AL158059 Human chr
C 804	16	8.8	139177	9	AC097060	Homo sapi	C 877	16	8.8	148704	9	AC123833	AC123833 Mus muscu
C 805	16	8.8	139628	2	AC095859	Human DNA	C 878	16	8.8	148704	9	AC124213	AC124213 Genomic s
C 806	16	8.8	139715	2	AC0127661	Rattus no	C 879	16	8.8	148894	9	AC126011	AC126011 Rattus no
C 807	16	8.8	139715	2	AC0127661	Rattus no	C 880	16	8.8	149035	2	AC0126011	AC0126011 Rattus no
C 808	16	8.8	140072	8	H0512B01	AC094867 Oryza sat	C 881	16	8.8	149405	2	AC0115271	AC0115271 Rattus no
C 809	16	8.8	140491	8	AC093276	Oryza sat	C 882	16	8.8	149437	2	AC027218	AC027218 Homo sapi
C 810	16	8.8	141281	2	AC018955	Mus muscu	C 883	16	8.8	149764	9	AC0087428	AC0087428 Homo sapi
C 811	16	8.8	141466	2	AC004863	Oryza sat	C 884	16	8.8	150017	2	AC002076	AC002076 Homo sapi
C 812	16	8.8	141466	2	AC004863	Oryza sat	C 885	16	8.8	150017	2	AC002076	AC002076 Homo sapi
C 813	16	8.8	141714	2	AC100353	Human DNA	C 886	16	8.8	150347	2	AC027038	AC027038 Oryza sat
C 814	16	8.8	141714	2	AC100353	Human DNA	C 887	16	8.8	150347	2	AC027038	AC027038 Oryza sat
C 815	16	8.8	141798	2	AC124283	Homo sapi	C 888	16	8.8	150429	9	AC012089	AC012089 Homo sapi
C 816	16	8.8	141798	2	AC124283	Homo sapi	C 889	16	8.8	150561	2	AC012089	AC012089 Homo sapi
C 817	16	8.8	141881	4	AC087421	Felis cat	C 890	16	8.8	150561	2	AC012089	AC012089 Homo sapi
C 818	16	8.8	142024	2	AC004705	Oryza sat	C 891	16	8.8	150646	9	AC068129	AC068129 Homo sapi
C 819	16	8.8	142192	2	AC015594	Homo sapi	C 892	16	8.8	150646	9	AC068129	AC068129 Homo sapi
C 820	16	8.8	142192	2	AC015594	Homo sapi	C 893	16	8.8	150652	2	AC016535	AC016535 Homo sapi
C 821	16	8.8	142568	2	AC033960	Homo sapi	C 894	16	8.8	150781	2	AC013964	AC013964 Mus muscu
C 822	16	8.8	142762	2	AC013959	Oryza sat	C 895	16	8.8	151132	9	AC012001	AC012001 Rattus no
C 823	16	8.8	142812	9	AC098617	Homo sapi	C 896	16	8.8	151146	2	AC011505	AC011505 Rattus no
C 824	16	8.8	142969	2	AC025840	Homo sapi	C 897	16	8.8	152366	9	AC102022	AC102022 Mus muscu
C 825	16	8.8	142969	2	AC025840	Homo sapi	C 898	16	8.8	152366	9	AC102022	AC102022 Mus muscu
C 826	16	8.8	143409	2	AC001787	Homo sapi	C 899	16	8.8	152706	9	AC008568	AC008568 Homo sapi
C 827	16	8.8	143446	2	AC005181	Oryza sat	C 900	16	8.8	152706	9	AC008568	AC008568 Homo sapi
C 828	16	8.8	143446	2	AC005181	Oryza sat	C 901	16	8.8	152742	2	AC022381	AC022381 Homo sapi
C 829	16	8.8	144038	2	AC135856	Homo sapi	C 902	16	8.8	153021	2	AC079214	AC079214 Homo sapi
C 830	16	8.8	144038	2	AC135856	Homo sapi	C 903	16	8.8	153021	2	AC079214	AC079214 Homo sapi
C 831	16	8.8	144449	2	AC067926	Mus muscu	C 904	16	8.8	153057	9	AC087091	AC087091 Homo sapi
C 832	16	8.8	144585	2	AC025736	Homo sapi	C 905	16	8.8	153141	9	AC087091	AC087091 Homo sapi
C 833	16	8.8	144651	8	AC025736	Homo sapi	C 906	16	8.8	153141	9	AC087091	AC087091 Homo sapi
C 834	16	8.8	145003	2	AC029187	Oryza sat	C 907	16	8.8	153258	2	AC026506	AC026506 Homo sapi
C 835	16	8.8	145003	2	AC029187	Oryza sat	C 908	16	8.8	153258	2	AC026506	AC026506 Homo sapi
C 836	16	8.8	145050	9	AC021078	Homo sapi	C 909	16	8.8	153886	2	AC016316	AC016316 Homo sapi
C 837	16	8.8	145192	9	AC063866	Human DNA	C 910	16	8.8	154138	2	AC013551	AC013551 Homo sapi
C 838	16	8.8	145267	2	AC109644	Oryza sat	C 911	16	8.8	154138	2	AC013551	AC013551 Homo sapi
C 839	16	8.8	145320	6	OS0200243	AL713500 Oryza sat	C 912	16	8.8	154138	2	AC013551	AC013551 Homo sapi
C 840	16	8.8	145414	2	AC1135519	Homo sapi	C 913	16	8.8	154256	2	AC095937	AC095937 Rattus no
C 841	16	8.8	145414	2	AC1135519	Homo sapi	C 914	16	8.8	154256	2	AC095937	AC095937 Rattus no
C 842	16	8.8	145450	2	AC068652	Homo sapi	C 915	16	8.8	154288	2	AC005494	AC005494 Mus muscu
C 843	16	8.8	145450	2	AC068652	Homo sapi	C 916	16	8.8	154301	9	AC005494	AC005494 Mus muscu
C 844	16	8.8	145457	2	AC024270	Oryza sat	C 917	16	8.8	154301	9	AC005494	AC005494 Mus muscu
C 845	16	8.8	145538	9	AP045GDI9	292542 Human DNA	C 918	16	8.8	154338	2	AC0115065	AC0115065 Mus muscu
C 846	16	8.8	145727	4	AC030027	Equine he	C 919	16	8.8	154413	2	AC009805	AC009805 Homo sapi
C 847	16	8.8	145844	9	AC004931	Homo sapi	C 920	16	8.8	154413	2	AC009805	AC009805 Homo sapi
C 848	16	8.8	145910	8	OS0300027	AL066600 Oryza sat	C 921	16	8.8	154682	9	AL159158	AL159158 Human DNA
C 849	16	8.8	145910	8	OS0300027	AL066600 Oryza sat	C 922	16	8.8	154746	9	AL157944	AL157944 Human DNA
C 850	16	8.8	145976	9	AC005474	Oryza sat	C 923	16	8.8	154840	2	AC032035	AC032035 Homo sapi
C 851	16	8.8	145976	9	AC005474	Oryza sat	C 924	16	8.8	155124	10	AL627406	AL627406 Mouse DNA
C 852	16	8.8	146095	10	AC117837	Mus muscu	C 925	16	8.8	155175	2	AC123386	AC123386 Rattus no
C 853	16	8.8	146310	2	AC116524	Mus muscu	C 926	16	8.8	155507	2	AC131747	AC131747 Dantio rer
C 854	16	8.8	146310	2	AC116524	Mus muscu	C 927	16	8.8	155507	2	AC131747	AC131747 Dantio rer
C 855	16	8.8	146394	9	AC081363	Homo sapi	C 928	16	8.8	155670	3	CEV39B4B	CEV39B4B Caenorhab
C 856	16	8.8	146394	9	AC081363	Homo sapi	C 929	16	8.8	155670	3	CEV39B4B	CEV39B4B Caenorhab
C 857	16	8.8	146425	2	AC005258	Oryza sat	C 930	16	8.8	155908	2	AC024218	AC024218 Homo sapi
C 858	16	8.8	146571	2	AC128276	Rattus no	C 931	16	8.8	156195	9	AC022806	AC022806 Homo sapi
C 859	16	8.8	146571	2	AC128276	Rattus no	C 932	16	8.8	156195	9	AC022806	AC022806 Homo sapi
C 860	16	8.8	146916	9	AC003755	Homo sapi	C 933	16	8.8	156228	2	AC0303799	AC0303799 Homo sapi
C 861	16	8.8	146916	9	AC003755	Homo sapi	C 934	16	8.8	156228	2	AC0303799	AC0303799 Homo sapi
C 862	16	8.8	147176	2	AC026014	Homo sapi	C 935	16	8.8	156491	9	AL591720	AL591720 Human DNA
C 863	16	8.8	147176	2	AC026014	Homo sapi	C 936	16	8.8	156491	9	AL591720	AL591720 Human DNA
C 864	16	8.8	147670	10	AC084020	Mus muscu	C 937	16	8.8	156508	2	AC004590	AC004590 Homo sapi
C 865	16	8.8	147826	9	AC001328	Homo sapi	C 938	16	8.8	156687	2	AC008428	AC008428 Oryza sat
C 866	16	8.8	147859	9	AC092993	Homo sapi	C 939	16	8.8	156707	9	AL14208	AL14208 Rattus no
C 867	16	8.8	147887	2	AC004234	Oryza sat	C 940	16	8.8	156785	2	AC018541	AC018541 Human DNA
C 868	16	8.8	148068	1	AB001488	Bacillus	C 941	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 869	16	8.8	148068	1	AB001488	Bacillus	C 942	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 870	16	8.8	148068	1	AB001488	Bacillus	C 943	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 871	16	8.8	148068	1	AB001488	Bacillus	C 944	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 872	16	8.8	148068	1	AB001488	Bacillus	C 945	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 873	16	8.8	148068	1	AB001488	Bacillus	C 946	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 874	16	8.8	148068	1	AB001488	Bacillus	C 947	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 875	16	8.8	148068	1	AB001488	Bacillus	C 948	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 876	16	8.8	148068	1	AB001488	Bacillus	C 949	16	8.8	156823	9	AC007572	AC007572 Drosophila
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C 878	16	8.8	148068	1	AB001488	Bacillus	C 951	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 879	16	8.8	148068	1	AB001488	Bacillus	C 952	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 880	16	8.8	148068	1	AB001488	Bacillus	C 953	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 881	16	8.8	148068	1	AB001488	Bacillus	C 954	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 882	16	8.8	148068	1	AB001488	Bacillus	C 955	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 883	16	8.8	148068	1	AB001488	Bacillus	C 956	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 884	16	8.8	148068	1	AB001488	Bacillus	C 957	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 885	16	8.8	148068	1	AB001488	Bacillus	C 958	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 886	16	8.8	148068	1	AB001488	Bacillus	C 959	16	8.8	156823	9	AC007572	AC007572 Drosophila
C 887	16												


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BASE COUNT      221 a 152 c 157 g
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e-93;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTCCGAGAGATTTTATTACTTAT 60
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Db 140 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 199

Qy 121 GCTGAGAACTTCTACTAGTATGTCATCTCTGACCTCATGCTGATGATTCGAATGTTCTCTTC 180
Db 200 GCTGAGAACTTCTACTAGTATGTCATCTCTGACCTCATGCTGATGATTCGAATGTTCTCTTC 259

Qy 181 A 181
Db 260 A 260

RESULT 3
AF071002
LOCUS      Homo sapiens mink-related peptide 1 mRNA, linear PRI 29-APR-1999
DEFINITION
ACCESSION  AF071002
VERSION    AF071002.1 GI:4704422
KEYWORDS   Homo sapiens
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 732)
AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
TITLES    Submitted (05-008-1999) Section of Developmental Biology and
Medicine, Yale University School of Medicine, 295 Congress Avenue,
Cell 97 (21), 175-187 (1999)
JOURNAL   99235979
MEDLINE   99235979
PUBMED    10219239
AUTHORS    2 (bases 1 to 732)
TITLES    Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
JOURNAL   Direct Submission
TITLES    Submitted (05-008-1999) Section of Developmental Biology and
Medicine, Yale University School of Medicine, 295 Congress Avenue,
New Haven, CT 06536, USA
FEATURES   Location/Qualifiers
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BASE COUNT      221 a 152 c 157 g 202 t

Qy 1 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTCCGAGAGATTTTATTACTTAT 60
Db 147 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTTCGAGAGATTTTATTACTTAT 206

Qy 61 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 120
Db 207 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 266

Query Match      100.0%; Score 181; DB 9; Length 809;
Best Local Similarity 100.0%; Pred. No. 5e-93;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTCCGAGAGATTTTATTACTTAT 60
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Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTCCGAGAGATTTTATTACTTAT 60
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Qy 61 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 120
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Qy 121 GCTGAGAACTTCTACTAGTATGTCATCTCTGACCTCATGCTGATGATTCGAATGTTCTCTTC 180
Db 200 GCTGAGAACTTCTACTAGTATGTCATCTCTGACCTCATGCTGATGATTCGAATGTTCTCTTC 259

Qy 181 A 181
Db 260 A 260

RESULT 4
AF302095
LOCUS      Homo sapiens voltage-gated K+ channel subunit MIRP1 (KONE2) mRNA,
complete cds.
ACCESSION  AF302095
VERSION    AF302095.1 GI:10121887
KEYWORDS   Homo sapiens
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 809)
AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
TITLES    Cloning of a human MIRP1 cDNA
JOURNAL   10121887
REFERENCE  2 (bases 1 to 809)
AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
TITLES    Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
Institut Recerca Oncologica, Avia. de Castelldefels Km 2,7,
L'Hospitalet de Llobregat, Barcelona 08907, Spain
FEATURES   Location/Qualifiers
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LEESKATHENIGAGFNSP#
BASE COUNT      247 a 172 c 189 g 200 t 1 others
ORIGIN

Query Match      100.0%; Score 181; DB 9; Length 809;
Best Local Similarity 100.0%; Pred. No. 5e-93;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTCCGAGAGATTTTATTACTTAT 60
Db 147 ACTTTATCCAAATTTTCACAGAGCGCTCGGAGAGCTCTTCGAGAGATTTTATTACTTAT 206

Qy 61 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 120
Db 207 ATGGAACAATTTGGCCGCGAGACACACACAGCTGAGCAAGCGCCCTCCAGACCAAGTTGAT 266

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QY 121 GCTGAGAACTCTTACTATGTCATCTGTATCTATCTGCTGATGTAATGGATGTTCTTTC 180
Db 267 CCTGAGAACTCTTACTATGTCATCTGTATCTATCTGCTGATGTAATGGATGTTCTTTC 326
QY 181 A 181
327 A 327

RESULT 5
AP000320 24608 bp DNA linear PRI 20-NOV-1999
LOCUS Homo sapiens genomic DNA, chromosome 21q22.1, D2S1226-AML region,
DEFINITION complete sequence.
ACCESSION AP000320
VERSION AP000320.1 GI:4835689
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:Q12C8.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;
Eukaryota; Euthera; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 24608)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
JOURNAL Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Gnomonic Sciences Center (GSC);
Kitsato Univ., 1-15-1 Kitsato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
PUBMED 9924121
COMMENT AP000320 is a part of the data (ACCESSION No. AP000165 -
The sequencing project is supported by Japan Science Technology
Corporation (JST) and The Institute of Physical and Chemical
Research (RIKEN).
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4,6e-93;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15762 ATGGACAATTGGCCGAGACACAGCGTCAGCAGAGCGCTCCGAGAGATTTAT 15821
QY 121 CTTGAGAACTCTTACTATGTCATCTGTATCTATCTGCTGATGTAATGGATGTTCTTTC 180
Db 15822 CTTGAGAACTCTTACTATGTCATCTGTATCTATCTGCTGATGTAATGGATGTTCTTTC 180
QY 181 A 181
15882 A 15882
RESULT 6
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LOCUS Homo sapiens genomic DNA, chromosome 21q22.1, D2S1226-AML region,
DEFINITION clone B2344F14-f5088, segment 3/9, complete sequence.
ACCESSION AP000167

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AP000052 100000 bp DNA linear PRI 20-NOV-1999
LOCUS Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
DEFINITION complete sequence.
ACCESSION AP000052
VERSION AP000052.1 GI:3132362
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:245P17-f4A4f_2.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euthera; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
JOURNAL Submitted (11-MAY-1999) Masahira Hattori, Kitasato University,
Department of Science, JST sequencing Laboratory, Kitasato 1-15-1,
Saitama-shi, Saitama-shi, Japan (E-mail:hggc@kitasato.ac.jp,
Tel:0427-78-9712, Fax:0427-78-9561)
PUBMED 9561
COMMENT This sequence is conducted by Kitasato University JST sequencing
Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
sequence is submitted by Human Genome Sequencing in Aius project of
JST.
FEATURES
source Location/Qualifiers
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BASE COUNT 27603 A 21934 C 22513 G 27950 T
ORIGIN
Query Match 100.0%; Score 181; DB 9; Length 100000;
Best Local Similarity 100.0%; Pred. No. 4.5e-93;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 1ACTTATTCATTTTCACAGAGCGTGGAGAGCGTCTCCGAGAGATTTTATTACTTAT 60
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QY 121 CTTGAGAACTCTTACTATGTCATCTGTATCTATCTGCTGATGTAATGGATGTTCTTTC 180
Db 80344 CTTGAGAACTCTTACTATGTCATCTGTATCTGCTGATGTAATGGATGTTCTTTC 80403
QY 181 A 181
80404 A 80404

RESULT 7
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LOCUS Homo sapiens genomic DNA, chromosome 21q22.1, D2S1226-AML region,
DEFINITION clone B2344F14-f5088, segment 3/9, complete sequence.
ACCESSION AP000167

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VERSION      AP000167.1  GI:4827132
KEYWORDS     HGC
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 100000)
CLONE RANGE: B2344F14-F50E8)
JOURNAL      Published Only in Database (1999)
REFERENCE    2 (bases 1 to 100000)
AUTHORS      Hattori M., Ishii K., Toyoda A., Taylor T.D., Hong-Seog P.,
TITLE        Fujiyama A., Yada T., Tokoi Y. and Sakaki Y.
JOURNAL      Submitted (15-APR-1999) to the EMBL/GenBank/DBJ databases
Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan
(E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/,
Tel:81-3-5214-8491, Fax:81-3-5214-8470)
[1]
RP      Hirakawa M., Yamaguchi H., Imai K., Shimada J.:
RA      1-100000
RL      Submitted (15-APR-1999) to the EMBL/GenBank/DBJ databases
Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan
(E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/,
Tel:81-3-5214-8491, Fax:81-3-5214-8470)
[2]
RP      Hattori M., Ishii K., Toyoda A., Shiba T., Sakaki Y.:
RA      "Homo sapiens B17.199bp genomic DNA of 21q22.1 GART and AML region";
RT      Unpublished.
XX      This sequence is conducted by Kitasato University JST sequencing
Laboratory as a JST sequencing team.
CC      Principal Investigator: Yoshiyuki Sakaki Ph.D.
CC      Email: yshi@kitasato.ac.jp, Tel: +81-3-5449-5445,
CC      Fax: +81-3-5449-5622, Fax: +81-3-5449-5445,
CC      Web: http://www.kitasato.ac.jp
CC      Sub-leader: Tadayoshi Shibuya Ph.D., Masahira Hattori Ph.D.
CC      The sequence is submitted by Human Genome Sequencing in ALIS
CC      project of JST.
CC      Japan Science and Technology Corporation (JST)
CC      5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
CC      For further information about this sequence, including its
CC      location and relationship to other sequences, please visit our
CC      website at http://www.kitasato.ac.jp/~webmaster/alis.tokyo.jst.go.jp
CC      or send email to webmaster@www-alis.tokyo.jst.go.jp
XX      Key      Location/Qualifiers
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FT      /organism="Homo sapiens"
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FT      /note="ATMA086yF9; Genethon Marker; The location is between
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QY      61      ATGCACATTTGGCCGACACACAGACGCTGACGAGAGGCGCTTCAGCCCAAGTTGAT 120
DB      89586  ATGCACATTTGGCCGACACACAGACGCTGACGAGAGGCGCTTCAGCCCAAGTTGAT 89645
QY      121     GCTGAGAACTTCTACTATGTCTCTGTACTCTGATCTGATGATGATGATGATGATGAT 180
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Qy 61 ATGACCAATTTGGGCGCAAGAACACACAGCTGAGCAAGAGCCCTCCAGCAAGTGTAT 120
Db 301493 ATGACCAATTTGGGCGCAAGAACACACAGCTGAGCAAGAGCCCTCCAGCAAGTGTAT 301552

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Qy 181 A 181
Db 301613 A 301613

RESULT 10
LOCUS AX406947 732 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 9 from Patent WO0222875.
ACCESSION AX406947
VERSION AX406947.1 GI:21439822
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goldstein,S.A.
TITLE Polymorphisms associated with cardiac arrhythmia
JOURNAL Patent: NO 0222875-A 9 21-MAR-2002;
YALE UNIVERSITY (US)
FEATURES
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location/Qualifiers
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variation
/notes="The drug associated here is was Bactrim."
BASE COUNT 220 a 152 c 158 g 202 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 165; DB 6; Length 732;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CACAGCGCTGGAAGAGCTCTTCGAGAGTTTATTTACTATATGAGCAATTCGGCC 76
Db 96 CACAGCGCTGGAAGAGCTCTTCGAGAGTTTATTTACTATATGAGCAATTCGGCC 155

Qy 77 AGAACACAACTGAGCAGAGAGGCCCTCCAAAGCTGATGCTGAGAGCTTCTACT 136
Db 156 AGAACACAACTGAGCAGAGAGGCCCTCCAAAGCTGATGCTGAGAGCTTCTACT 215

Qy 137 ATGTATCTCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 181
Db 216 ATGTATCTCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 260

RESULT 11
LOCUS AX406945 732 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 7 from Patent WO0222875.
ACCESSION AX406945
VERSION AX406945.1 GI:21439820
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goldstein,S.A.

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TITLE Polymorphisms associated with cardiac arrhythmia
JOURNAL Patent: MO 0222875-A 7 21-MAR-2002;
YALE UNIVERSITY (US)
FEATURES Location/Qualifiers
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/note="mink-related peptide 1, Thr substituted for Ile at amino acid 57"
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variation 1..732
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BASE COUNT 221 a 153 c 157 g 201 t
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Query Match 90.1%; Score 163; DB 6; Length 732;
Best Local Similarity 100.0%; Pred. No. 1.2e-82;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACTTATCCATTTCCACAGAGCGTGGAGAGCTCTTCGAGAGATTTTATTACTTAT 60
DB 80 ACTTATCCATTTCCACAGAGCGTGGAGAGCTCTTCGAGAGATTTTATTACTTAT 139
QY 61 ATGGACAATTTGGCGGACAGACACAGCTGAGCAAGAGGCCCTCCAGCCAAAGTTGAT 120
DB 140 ATGGACAATTTGGCGGACAGACACAGCTGAGCAAGAGGCCCTCCAGCCAAAGTTGAT 199
QY 121 GCTGAGACCTTCTATGATCTCTCTGATCTGATGATGATGATGATGATGATGAT 163
DB 200 GCTGAGACCTTCTATGATCTCTCTGATCTGATGATGATGATGATGATGATGAT 242
RESULT 12
LOCUS AX406943 732 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 5 from Patent MO0222875.
AUTHORS Goldstein, S.A.
TITLE Polymorphisms associated with cardiac arrhythmia
JOURNAL Patent: MO 0222875-A 5 21-MAR-2002;
YALE UNIVERSITY (US)
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TITLE Polymorphisms associated with cardiac arrhythmia
JOURNAL Patent: MO 0222875-A 7 21-MAR-2002;
YALE UNIVERSITY (US)
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ORIGIN

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QY 1 ACTTATCCATTTCCACAGAGCGTGGAGAGCTCTTCGAGAGATTTTATTACTTAT 60
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QY 61 ATGGACAATTTGGCGGACAGACACAGCTGAGCAAGAGGCCCTCCAGCCAAAGTTGAT 120
DB 140 ATGGACAATTTGGCGGACAGACACAGCTGAGCAAGAGGCCCTCCAGCCAAAGTTGAT 199
QY 121 GCTGAGACCTTCTATGATCTCTCTGATCTGATGATGATGATGATGATGATGAT 154
DB 200 GCTGAGACCTTCTATGATCTCTCTGATCTGATGATGATGATGATGATGATGAT 233
RESULT 13
LOCUS AY050513 372 bp mRNA linear ROD 15-OCT-2001
DEFINITION C. parvulus mink-related peptide 1 mRNA, complete cds.
AUTHORS Jiang, M., Zhang, M., Liu, J. and Tseng, G.-N.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-2001) Physiology, Virginia Commonwealth University, 1101 East Marshall Street, Richmond, VA 23298, USA
FEATURES Location/Qualifiers
source 1..372
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NFYVILVMVMIGMFATFVAILVSTVSKSRHSQDPYHOVIVEDMCKYRSQILH
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BASE COUNT 95 a 98 c 105 g 74 t
ORIGIN

Query Match 14.4%; Score 26; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 145 GTCATCTCTTACCTCATGGTGATGAT 170
RESULT 14
LOCUS AF071003 468 bp mRNA linear ROD 29-APR-1999
DEFINITION Rattus norvegicus mink-related peptide 1 mRNA, complete cds.
AUTHORS AF071003
ACCESSION AF071003.1 GI:4704424
VERSION AF071003.1
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 468)


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                    /clone="CH230-409A1"

BASE COUNT          36065 a 34436 c 33378 g 36487 t 4353 others
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Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

Oy 139 GTGATCTCTACTGATGTCATGTCATGAT 164
Db 131572 GTGATCTCTACTGATGTCATGTCATGAT 131547

RESULT 17
AF329636
LOCUS               AF329636
DEFINITION          Pacemaker channel beta subunit mirp1
ACCESSION           AF329636
VERSION             AF329636.1
KEYWORDS            GI:13194729
SOURCE              Oryctolagus cuniculus
ORGANISM            Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
REFERENCE           1. (bases 1 to 215)
AUTHORS             Wu, J., Potapova, I., Wymore, R. T., Holmes, B., Zuckerman, J.,
                    Zuckerman, T., Hwang, Z., Wang, H., Shi, W., Robinson, J., Ben-
                    jamin, W., Dixon, J. E., McKinnon, D. and Cohen, I. S.
                    Mink-related peptide 1: A beta subunit for the HCN ion channel
                    subunit family enhances expression and speeds activation
                    Circ. Res. 88 (12), E84-E87 (2001)
JOURNAL             21333430
MEDLINE             21333430
PUBMED              11470311
REFERENCE           1. (bases 1 to 215)
AUTHORS             Wymore, R. T., Hwang, Z., Wang, H., Shi, W., Robinson, J.,
                    Benjamin, W., Dixon, J. E., McKinnon, D. and Cohen, I. S.
                    Direct Submission
TITLE               Submitted (15-DEC-2000) Biology, The University of Tulsa, 600 S.
                    College Av., Tulsa, OK 74104-3189, USA
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BASE COUNT          60 a 58 c 51 g 46 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.066; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Oy 154 ATGTCGATGATGGAATGTCCT 176
Db 37 ATGTCGATGATGGAATGTCCT 59

RESULT 19
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LOCUS               AF387764
DEFINITION          Equus caballus mink related peptide 1-like mRNA, partial sequence.
ACCESSION           AF387764
VERSION             AF387764.1
KEYWORDS            GI:16797919
SOURCE              Equus caballus
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE           1. (bases 1 to 228)
AUTHORS             Stanley, M.R., Mitchell, K.E., Mitchell, B.M. and Freeman, L.C.
                    FASEB J. 15, 13135 (2001)
JOURNAL             2 (bases 1 to 228)
MEDLINE             2 (bases 1 to 228)
PUBMED              Finley, M.R., Li, Y. and Freeman, L.C.
                    Direct Submission
TITLE               Submitted (31-MAY-2001) Department of Anatomy and Physiology,
                    Kansas State University, 1600 Denison Ave, Manhattan, KS 66506, USA
                    NCBI staff are still waiting for submitters to provide appropriate
                    coding sequence information.
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                    /tissue_type="atrium"
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misc_feature

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```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.bhgc.bcm.tmc.edu/
Contact: bhgc-help@bcm.tmc.edu
----- Project Information
-----
Center project name: GPCX
Center clone name: CH230-159X5
Sequencing strategy: Plasmid
Sequencing vector: pBluescript
Chemistry: Dye-terminator Big Dye; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 17932 bases at least Q40
Consensus quality: 19302 bases at least Q30
Consensus quality: 20254 bases at least Q20

** NOTE: Exon-intron insert size may differ from sequence length
(see http://www.bcm.tmc.edu/GenomeCenter/GenData.html).
** NOTE: This is a "working draft" sequence. It currently
consists of 50 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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1616 1715: gap of unknown length
1716 2945: contig of 1230 bp in length
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3046 4078: contig of 1033 bp in length
4079 4178: gap of unknown length
4179 5226: contig of 1348 bp in length
5227 5527 6117: contig of 1091 bp in length
6118 6817: gap of unknown length
6818 7843: contig of 1026 bp in length
7844 7943: gap of unknown length
7944 9033: contig of 1090 bp in length
9034 9133: gap of unknown length
9133 10925: contig of 1532 bp in length
10926 12206: contig of 1381 bp in length
12207 12306: gap of unknown length
12307 13744: contig of 1438 bp in length
13745 13844: gap of unknown length
13845 15153: contig of 1309 bp in length
15154 15253: gap of unknown length
15254 16448: contig of 1195 bp in length
16449 17818: contig of 1270 bp in length
17819 17918: gap of unknown length
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/db_xref="taxon:10116"

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/clone="CH230-159X5"

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Best Local Similarity 100.0%; Pred.No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 CGAAGGCGCCCTCCAGCA 112

Db 13464 CGAAGGCGCCCTCCAGCA 13483

RESULT 23

AC108558/c

LOCUS AC108558 169873 bp DNA linear HTG 13-JUL-2002
DEFINITION Rattus norvegicus clone CH230-116N1, +... SEQUENCING IN PROGRESS

Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
 Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
 Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
 Earhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Giller,
 Gorrell, J. H., Guevara, M., Guzman, P., Haile, S., Hamilton, K.,
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Umanai K., Vaquez L., Vera, V., Villalton, D., Vinson, R., Wang Q.,
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Will, S., Williams, G., Winkler, R., Winkler, R., Winkler, R.,
Wu, C., Wu, Y., Wu, Y.F., Zhou J., Zorrilla, S., Neilson, D.,
Weinstock, G. and Gibbs R.
Direct Submission

Unpublished
 (bases 1 to 164995)
 Worley K.C.
 Direct Submission
 Submitted (08-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 164995)
 Worley, K. C.
 Direct Submission
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:17973833.
 ----- Genome Center
 Center: Baylor College of Medicine

```

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----
Center project name: GNP
Center clone name: CH230-178A23
Sequencing Summary Statistics
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 108374 bases at least Q40
Consensus quality: 114597 bases at least Q30
Consensus quality: 120549 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
      (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_read\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  * consists of 61 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * 'N' characters. The length of the gaps is unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.

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[illegible]

* NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. The sequence is available and the accession number will be preserved.

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* 2256	2355:	gap of unknown length
* 2356	3378:	contig of 1023 bp in length
* 3379	3478:	gap of unknown length
* 3479	5064:	contig of 1586 bp in length
* 5065	5164:	gap of unknown length
* 5165	6592:	contig of 1328 bp in length
* 6593	6592:	gap of unknown length
* 6593	7741:	contig of 1149 bp in length
* 7742	7841:	gap of unknown length
* 7842	9078:	contig of 1237 bp in length
* 9079	9179:	gap of unknown length
* 9179	10182:	contig of 1004 bp in length
* 10183	10282:	gap of unknown length
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* 13115	14445:	contig of 1331 bp in length
* 14446	14545:	gap of unknown length
* 14545	15626:	contig of 1081 bp in length

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 17527 17725: contig of 1999 bp in length
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 20018 21112: contig of 1195 bp in length
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Query Match 10.54; Score 19; DB 2; Length 176036;
 Recs Local Similarity 100.0%; Field No. 12; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

QY 41 GAAGCATTTTTTACTTAA 59
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RESULT 35
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 LOCUS
 DEFINITION Rattus norvegicus clone CH230-89B16, *** SEQUENCING IN PROGRESS
 AC127774 180153 bp DNA linear HTG 19-JUL-2002
 ***, 59 unordered pieces.
 AC127774 GI:21908146
 HTG: HTGS_PHASE1.
 SOURCE Rattus norvegicus
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buthera; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 1 (bases 1 to 180153)
 Murny D.M., Adams C., Adio-Oduola B., Ali-oman, F.R., Allen C.,
 Bousquet J., Boudreau J., Boudreau J., Boudreau J., Boudreau J.,
 Bouck J., Bowie S., Brivaga, K., Blankenburg K., Bonnin D.,
 Buhatz C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
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 Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos, C.,
 Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
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 Deucharte K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
 Earhart C., Edgar D., Edwards C.C., Elhaj C., Escotto M.,
 Faller T., Ferraguto D., Flagg N., Ford J.J., Foster P., Frantz P.,
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 Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Louieged, H.,
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 Nguyen N., Nickerson E., Nwokwkw, S., Ogih M., Okuwonu G.,
 Oragunye N., Oviedo R., Pace A., Payton B., Peery J., Perez L.,
 Peters L., Pickens R., Primus E., Pu L.L., Quiles M., Ren Y.,
 Rives M., Rojase, A., Rojibokan I., Rolfe M., Ruiz S., Savery G.,

Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
 Stargren, S., Somaake, A., Spierke, A., Stanley, H., Stone, H.,
 Tansey, J., Taylor, C., Taylor, P., Thomas, K., Thomas, S.,
 Umanai, K., Vazquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G., and Gibbs, R.
 NCBI Human Genome Mission
 Unpublished
 2 (bases 1 to 180153)
 Worley, K.C.
 Direct Submission
 Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

 Project: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

 Center project name: G25Q
 Center accession name: G25Q-89816
 Center clone name: G25Q-89816

 Sequencing vector: Plasmid:
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 132310 bases at least Q40
 Consensus quality: 140812 bases at least Q30
 Consensus quality: 146966 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 59 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1421 1420: contig of 1420 bp in length
 * 1421 1520: gap of unknown length
 * 1521 2331: contig of 1411 bp in length
 * 2332 3031: gap of unknown length
 * 3032 4421: contig of 1390 bp in length
 * 4422 5501: gap of unknown length
 * 5502 6002: gap of unknown length
 * 6003 7241: contig of 1239 bp in length
 * 7242 7341: gap of unknown length
 * 7342 9500: contig of 2159 bp in length
 * 9501 9600: gap of unknown length
 * 9601 10546: contig of 1046 bp in length
 * 10547 11636: gap of unknown length
 * 11637 11930: gap of unknown length
 * 11931 13178: contig of 1248 bp in length
 * 13179 13278: gap of unknown length
 * 13279 14730: contig of 1452 bp in length
 * 14731 14830: gap of unknown length
 * 14831 16464: contig of 1634 bp in length
 * 16465 18208: gap of unknown length
 * 18209 18308: gap of unknown length
 * 18310 20250: contig of 1941 bp in length
 * 20251 20350: gap of unknown length
 * 20351 21750: contig of 1400 bp in length
 * 21751 21850: gap of unknown length
 * 21851 23381: contig of 1531 bp in length
 * 23382 23481: gap of unknown length
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 * 23482 24653: contig of 1172 bp in length
 * 24654 24751: gap of unknown length
 * 24752 26273: gap of unknown length
 * 26274 27958: contig of 1685 bp in length
 * 27959 28058: gap of unknown length
 * 28059 29402: contig of 1344 bp in length
 * 29403 31187: contig of 1685 bp in length
 * 31188 31602: gap of unknown length
 * 31603 33142: gap of unknown length
 * 33143 35128: contig of 1986 bp in length
 * 35129 35228: gap of unknown length
 * 35229 38085: contig of 2857 bp in length
 * 38086 38185: gap of unknown length
 * 38186 39781: contig of 1596 bp in length
 * 39782 42266: gap of unknown length
 * 42267 42366: gap of unknown length
 * 42367 43566: contig of 1200 bp in length
 * 43567 43666: gap of unknown length
 * 43667 45411: contig of 1745 bp in length
 * 45412 45511: gap of unknown length
 * 45512 47033: contig of 1522 bp in length
 * 47034 49387: gap of unknown length
 * 49388 49487: gap of unknown length
 * 49488 51080: contig of 1593 bp in length
 * 51081 51180: gap of unknown length
 * 51181 53455: contig of 2275 bp in length
 * 53456 53555: gap of unknown length
 * 53556 55259: contig of 2004 bp in length
 * 55260 58027: gap of unknown length
 * 58028 58107: gap of unknown length
 * 58108 61502: contig of 3395 bp in length
 * 61503 61602: gap of unknown length
 * 61603 63437: contig of 1835 bp in length
 * 63438 63537: gap of unknown length
 * 63538 65288: contig of 2751 bp in length
 * 65289 68546: gap of unknown length
 * 68547 68646: gap of unknown length
 * 68647 73537: contig of 4891 bp in length
 * 73538 73637: gap of unknown length
 * 73638 77125: contig of 3488 bp in length
 * 77126 77225: gap of unknown length
 * 77226 80563: contig of 3338 bp in length
 * 80564 83984: contig of 3321 bp in length
 * 83985 84084: gap of unknown length
 * 84085 87419: contig of 3335 bp in length
 * 87420 87519: gap of unknown length
 * 87520 91100: contig of 3581 bp in length
 * 91101 91200: gap of unknown length
 * 91201 92131: contig of 3931 bp in length
 * 92132 93154: gap of unknown length
 * 93155 98454: gap of unknown length
 * 98455 104119: contig of 5665 bp in length
 * 104120 104219: gap of unknown length
 * 104220 107789: contig of 3570 bp in length
 * 107790 107889: gap of unknown length
 * 107890 111284: contig of 3695 bp in length
 * 111285 115667: contig of 4883 bp in length
 * 115668 116667: gap of unknown length
 * 116668 119994: contig of 3327 bp in length
 * 119995 120094: gap of unknown length
 * 120095 124984: contig of 4890 bp in length
 * 124985 125084: gap of unknown length
 * 125085 129333: contig of 4449 bp in length

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

* 125756 gap of unknown length
* 125757 gap of unknown length
* 130912 gap of unknown length
* 130913 contig of 7338 bp in length
* 130913 138250: contig of 7338 bp in length
* 138251 138250: gap of unknown length
* 138251 148729: contig of 10379 bp in length
* 148730 148829: gap of unknown length
* 148730 158131: contig of 9302 bp in length
* 148730 158231: gap of unknown length
* 158232 158231: gap of unknown length
* 173849 173948: gap of unknown length
* 173949 175348: contig of 1400 bp in length
* 175349 175448: gap of unknown length
* 175449 176535: contig of 1087 bp in length
* 176536 176635: gap of unknown length
* 176636 178205: contig of 1570 bp in length
* 178206 179251: gap of unknown length
* 179252 179535: gap of unknown length
* 179536 179853: gap of unknown length
* 179854 181517: contig of 1664 bp in length
* 181518 181517: gap of unknown length
* 181518 183178: contig of 1561 bp in length.

FEATURES

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/organism="Homo sapiens"
/chromosome="17"
/clone="RP11-68105"

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misc_feature 1667..2772

misc_feature 2873..5020

misc_feature 5126..7358

misc_feature 7459..9055

misc_feature 9156..12153

misc_feature 12254..136742

misc_feature 13743..15772

misc_feature 15873..18136

misc_feature 18237..20007

misc_feature 20108..22021

misc_feature 22303..25427

misc_feature 25528..29038

misc_feature 29139..32005

misc_feature 32108..34657

misc_feature 34958..37234

misc_feature 37335..39701

misc_feature 39802..42193

misc_feature 42294..44856

misc_feature 44957..45485

misc_feature 45586..48182

misc_feature 48293..51587

misc_feature /note="assembly_name:Contig123"
51686..55267
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55267..58902

Query Match 10.5%; Score 19; DB 2; Length 183178;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 CAAAGTCTGATCTGAGAAC 129

Db 24459 CAAAGTCTGATCTGAGAAC 24477

RESULT 37

AC073162 AC073162 185754 bp DNA linear PRI 26-APR-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-536724, complete sequence.
ACCESSION AC073162
VERSION AC073162.9 GI:20330787
KEYWORDS HTG.
SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Smith,D.R.
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
UNPUBLISHED

REFERENCE 2 (bases 1 to 185754)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (06-APR-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA

REFERENCE 3 (bases 1 to 185754)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA

REFERENCE 4 (bases 1 to 185754)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (06-APR-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA

REMARK 1329 bases of Tn10 (J01829) transposon removed here
COMMENT On Apr 26, 2002 this sequence version replaced gi:20066186.
FEATURES
Location/Qualifiers
1..185754 Homo sapiens
/organism="Homo sapiens"
/db="taxon:9606"
/chromosome="10"
/clone="RP11-536724"
/clone.lib="RP11-11"

BASE COUNT 61914 a 38909 c 36605 g 48326 t
ORIGIN
Query Match 10.5%; Score 19; DB 9; Length 185754;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTATTACTTATGAGCA 67

Db 13249 TTATTACTTATGAGCA 13267

RESULT 38

AC06281 AC06281 199551 bp DNA linear HTG 12-AUG-2000
DEFINITION Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
ACCESSION AC06281
VERSION AC06281.8 GI:9797738

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KEYWORDS      HTG; HTGS PHASE1.
SOURCE         Plasmodium falciparum.
ORGANISM       Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
REFERENCE      1 (bases 1 to 199551) Qin F., Bowley D., Mao J., Tamaki, T.,
AUTHORS        Kurdi, O.B., Chung, E. L., B. and Davis, R.W.
TITLE          Plasmodium falciparum 3D7 chromosome 12
JOURNAL         Unpublished
REFERENCE      2 (bases 1 to 199551)
AUTHORS        Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
TITLE          Direct Submission
JOURNAL         Submitted (05-JUN-1999) Stanford DNA Sequencing and Technology
                94104, USA: Stanford University, 835 California Avenue, Palo Alto, CA
COMMENT        * NOTE: This is a 'working draft' sequence. It currently
                * consists of 2 contigs. The true order of the pieces
                * is not known and their order in this sequence record is
                * arbitrary. Gaps between the contigs are represented as
                * this C1. But the exact size of the gaps are unknown.
                * This C1 may be extended with the following contigs:
                * as soon as it is available and the accession number will
                * be preserved.
                * 1 41526: contig of 41526 bp in length
                * 41527 41726: gap of unknown length
                * 41727 199551: contig of 157825 bp in length.
FEATURES       Location/Qualifiers
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                repeat_region   /db_xref="taxon:5833"
                repeat_region   /chromosome="12"
                repeat_region   /clones="PFYACB8-95"
                repeat_region   /clones="3D7"
BASE COUNT     83197 A 17543 C 19759 G 78852 T 200 others
ORIGIN
Query Match      10.5%; Score 19; DB 2; Length 199551;
Beat Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative
QY              46 ATTTTATTACTTATGCG 64
DB              66147 ATTTTATTACTTATGCG 66129

RESULT 39
HUA000659
LOCUS          HUA000659      251199 bp      DNA      linear      PRI 15-JUN-2001
DEFINITION     Homo sapiens T-cell receptor alpha delta locus from bases 250472 to
                501670 (section 2 of 5) of the Complete Nucleotide Sequence.
ACCESSION      AE000659.1
VERSION        AE000659.1 GI:2335023
KEYWORDS       Homo sapiens.
SOURCE         Homo sapiens.
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 251199) Hsu K., Kuo C.L., Sato, D., Lensara, J.A.,
AUTHORS        Kopp, S., Shaw, M., Deshpande, P. and Hood L.
TITLE          The human T-cell receptor TCRAC/TCRDC (C alpha/C delta) region:
                organization, sequence, and evolution of 97.6 kb of DNA
                Genomics 19 (3), 478-493 (1994)
JOURNAL         Genomics 19 (3), 478-493 (1994)
MEDLINE        94245236
PUBMED         8188290
REMARKS        This citation covers from bases 963183-1064019
REFERENCE      2 (bases 1 to 251199) Hsu K., Kuo C.L., Sato, D., Lensara, J.A.,
AUTHORS        Kopp, S., Shaw, M., Deshpande, P. and Hood L.
TITLE          Analysis of the 1.1-Mb human alpha/delta T-cell receptor locus with
                bacterial artificial chromosome clones
                Genome Res. 7 (4), 330-338 (1997)
JOURNAL         Genome Res. 7 (4), 330-338 (1997)
MEDLINE        97264339

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PUBMED         9110172
REFERENCE      3 (bases 1 to 251199)
AUTHORS        Boyesen, C., Inouy, L., Smith, T.M., Smit, A., Meng, X., Rowen, L. and
                Hood, L.
TITLE          T-Cell Receptor Alpha Delta Locus Complete Nucleotide Sequence
                TCRAD
JOURNAL         Submitted (05-JUN-1999) Stanford DNA Sequencing and Technology
                94104, USA: Stanford University, 835 California Avenue, Palo Alto, CA
REMARK        This citation covers bases 1-983545 and bases 1064020-1071650
REFERENCE      4 (bases 1 to 251199)
AUTHORS        Boyesen, C., Lee, I., Smith, T.M., Smit, A., Kai, W., Lee, R. and Leroy, H.
TITLE          Direct Submission
JOURNAL         Submitted (20-JUL-1997) Department of Molecular Biotechnology,
                University of Washington, Box 357730, Seattle, Washington 98195,
                USA
REMARK        Complete nucleotide sequence of the human T-cell receptor alpha
                delta locus
                On Jun 12, 2001 this sequence version replaced GI:2766593.
                Sequencing method: high redundancy shotgun. Interspersed Repeats
                were identified with RepeatMasker (available from
                http://ftp.genome.washington.edu/RM/RepeatMasker.html) Simple
                sequence repeats were identified with sputnik (available from
                http://seccr.fhcg.utah.edu/~chrisa/software/sputnik.html).
FEATURES       Location/Qualifiers
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                source          /db_xref="taxon:9606"
                source          33706..138937
                source          /organism="Homo sapiens"
                source          /db_xref="taxon:9606"
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                repeat_region   /TPT_family="L1"
                repeat_region   /TPT_family="AluSp"
                repeat_region   1711..1791
                repeat_region   /TPT_family="MERSA"
                repeat_region   /TPT_family="MER20"
                gene            4449..5201
                gene            /gene="TCRAV5S1"
                promoter        4449..4468
                promoter        /gene="TCRAV5S1"
                promoter        /standard_name="TCRAV5S1"
                mRNA            4449..4698,4875..5162
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                CDS             /standard_name="TCRAV5S1"
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                CDS             /db_xref="GI:2335026"
                CDS             /translation="MKTTFAGSFLEFLMQDCMGRGEVDSFLSVREGDSVINCT
                YDSSSTLYWYKQVEPAGLQGLUTIFSNNDKQDRLVLLKKDKHLSTADTOT
                GDSATFCAGS 4698,4875..5162)
                V_segment      4698..4875
                V_segment      /gene="TCRAV5S1"
                V_segment      /standard_name="TCRAV5S1"
                V_segment      /note="Old name TCRAV15S1"
                misc_recomb     5163..5169
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                misc_recomb     /standard_name="TCRAV5S1"
                misc_recomb     /note="Repeatmer"
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                misc_recomb     /standard_name="TCRAV5S1"
                misc_recomb     /note="Repeatmer"
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                misc_recomb     /standard_name="TCRAV5S1"
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repeat_region	/standard_name="TCRAV6S1"	/note="nonamer"	5630..5724	/rpt_family="MER4_internal"	complement(7864..8152)	/rpt_family="AluX"	9253..9262 tandem	8886..8892	/rpt_unit="ATC"	/rpt_type="tandem"	/rpt_unit="TTTA"	complement(8895..9195)	/rpt_family="AluSX"	/rpt_family="L1P4_send"	10101..11383	/rpt_family="L1"	complement(11565..11901)	/rpt_family="L1P4"	complement(11892..12127)	/rpt_family="L1P3"	complement(12119..15338)	/rpt_family="L1"	15339..15381	/rpt_family="AluXB"	15531..20950	/rpt_family="L1"	20801..21692	/rpt_family="L1P4"	complement(22178)	/rpt_family="L1P2"	23528..23680	/rpt_family="MER5A"	/gene="TCRAV6S1"	23719..24532	/gene="TCRAV6S1"	23719..23738	/gene="TCRAV6S1"	/note="Old name TCRAV6S1"	/note="Old name TCRAV6S1"	join(<23966..24017,24206..>24493)	/product="TCRAV6S1"	/notes="Old name TCRAV6S1"	join(23966..24017,24206..>24493)	/standard_name="TCRAV6S1"	/note="Old name TCRAV6S1"	/codon_start=1	/product="TCRAV6S1"	/protein_xref="P3586003.1"	/db_xref="GI:23580207"	/translation="MESFGLGVLLILMLQVWVKSQIFONSALMIDEGKATLTCNADSNATYGLCLD"	ADSNATYGLCLD	join(23966..24017,24206..>24493)	/standard_name="TCRAV6S1"	/note="Old name TCRAV6S1"	24494..24500	/gene="TCRAV6S1"	/note="Old name TCRAV6S1"	24501..24523	/note="Old name TCRAV6S1"	/gene="TCRAV6S1"	/standard_name="TCRAV6S1"	/note="spacer"	24524..24532	/gene="TCRAV6S1"	/note="nonamer"	complement(25031..25204)	/rpt_family="AluX"	repeat_region

repeat_region	/standard_name="TCRAV6S1"	/note="nonamer"	5630..5724	/rpt_family="MER4_internal"	complement(7864..8152)	/rpt_family="AluX"	9253..9262 tandem	8886..8892	/rpt_unit="ATC"	/rpt_type="tandem"	/rpt_unit="TTTA"	complement(8895..9195)	/rpt_family="AluSX"	9101..9110	/rpt_family="L1P4_send"	10101..11383	/rpt_family="L1"	complement(11565..11901)	/rpt_family="L1P4"	complement(11892..12127)	/rpt_family="L1P3"	complement(12119..15338)	/rpt_family="L1"	15339..15381	/rpt_family="AluXB"	15531..20950	/rpt_family="L1"	20801..21692	/rpt_family="L1P4"	complement(22118)	/rpt_family="L1P2"	23528..23680	/rpt_family="MER5A"	23719..24532	/gene="TCRAV6S1"	23719..23738	/gene="TCRAV6S1"	/note="Old name TCRAV6S1"	/note="Old name TCRAV6S1"	/product="TCRAV6S1"	/notes="Old name TCRAV6S1"	join(21966..24017,24206..24493)	/standard_name="TCRAV6S1"	/note="Old name TCRAV6S1"	/codon_start=1	/product="TCRAV6S1"	/protein_xref="GI:2358002.1"	/translation="MESFUGVLLILMLQVWVKSKI FONS EALMIGKATLTCN ADANATYCLGLD"	ADANATYCLGLD	join(23966..24017,24206..24493)	/standard_name="TCRAV6S1"	/note="Old name TCRAV6S1"	24494..24500	/gene="TCRAV6S1"	/note="Old name TCRAV6S1"	/product="TCRAV6S1"	24501..24523	/gene="TCRAV6S1"	/standard_name="TCRAV6S1"	/note="spacer"	24524..24532	/gene="TCRAV6S1"	/note="nonamer"	complement(25031..25204)	/rpt_family="AluX"	repeat_region																					
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BASE COUNT 95 a 90 c 99 g 136 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 39 CCGAGGAGTTTATTAC 56
DB 273 CCGAGGAGTTTATTAC 256

RESULT 41
G39242/c
LOCUS Z20324 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
DEFINITION G39242
ACCESSION G39242.1 GI:3358451
VERSION 1
KEYWORDS STS, 90 c, 99 g, 136 t
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Shimoda, N., Knäpik, E.W., Zintzi, J., Sim, C., Yamada, E., Kaplan, S.,
Jackson, D., de Sauvage, F.H., and Fishman, M.C.
Genomic organization of the 3000 microsatellite markers
Genomics 58 (3), 219-232 (1999)
99303552
10373319

Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail Code 149A100R, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishman@cvc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: GTGGGTGAACAGCTGGG
Primer B: TGGAGGATCATCTGAACCC
STS size: 138
PCR
Primer: 94 degrees C for 5.0 minutes
Denaturation: 94 degrees C for 1.0 minute
Annealing: 58 degrees C for 1.0 minute
Polymerization: 72 degrees C for 1.5 minute
PCR Cycles: 27
Thermal Cycler: MJ Research PTC-100
Protocol:
10 PB
Reagents: each 375 nM
dNTPs: each 200 uM
Taq Polymerase: 0.034 units/u1
Total Vol: 10 u1
Buffer: MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

Primers are available from Research Genetics Inc.
(http://www.regen.com phone: 800-533-4363).

```

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FEATURES
source
Location/Qualifiers
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/organism="Danio rerio"
/strain="AB"
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/lab_host="DH5alpha"
/notes="Vector: m13mp19 with added BarXI site. V-type:
Phage; Genomic DNA from a single adult Zebrafish (AB
strain) was digested with BamHI and SalI, and the
resulting fragments in the range of 250-500 bp were gel
purified and a BarXI linker was added. The fragments were
cloned into a modified m13mp19 vector and transcribed
into E. Coli DH5alpha. Microsatellite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
probes."
STS
137..274
Primer_bind
137..274
Primer_bind
137..274
Primer_bind
BASE COUNT 124 a 117 c 218 g 183 t 17 others
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Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 74 GCCAGACACACACGCTG 91
DB 88 GCCAGACACACACGCTG 71

RESULT 42
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DEFINITION Human ataxia-telangiectasia (ATM) gene, exon 36.
ACCESSION U55733.1
VERSION U55733.1 GI:1497905
KEYWORDS ataxia-telangiectasia
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 750)
Rasio, D., Negri, M. and Croce, C.M.
Genomic organization of the ATM locus involved in
ataxia-telangiectasia
Cancer Res. 55 (24), 6053-6057 (1995)
JOURNAL
15073130
PUBMED
8521392
REFERENCE 2 (bases 1 to 750)
Vorechovsky, I., Rasio, D., Luo, L., Monaco, C., Hammarstrom, L.,
Webster, A.D.B., Zaloudik, J., Barbanti-Brodano, G., James, M.,
Russo, G., Croce, C.M. and Negri, M.
The ATM gene and susceptibility to breast cancer: analysis of 38
breast tumors reveals no evidence for mutation
Cancer Res. 56 (12), 2726-2732 (1996)
JOURNAL
8665503
PUBMED
8665503
REFERENCE 3 (bases 1 to 750)
Negri, M., Rasio, D.
Direct Submission
AUTHORS
TITLE
JOURNAL
COMMENT
On Aug 21, 1996 this sequence version replaced gi:1165484.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity						
Matches						
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DEFINITION	Sequence 1611 from Patent WO0228891.					
ACCESSION	AX1414620					
VERSION	AX1414620.1		GI:21447077			
KEYWORDS	Listeria monocytogenes ATCC 19115.					
SOURCE	L. monocytogenes ATCC 19115					
ORGANISM	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.					
REFERENCE	1 Glaser, P. and Kunat, F.					
AUTHORS	Listeria innocua, genome and applications					
TITLE	Patent: WO 0228891-A 1611 11-APR-2002;					
JOURNAL	Pasteur Institute (FR)					
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ORIGIN						
Query Match						
Best Local Similarity						
Matches						
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RESULT 44						
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DEFINITION	P-gingivalis hagC gene encoding HagC hemagglutinin protein.					
ACCESSION	Z27394					
VERSION	Z27394.1		GI:510187			
KEYWORDS	hagC gene; hemagglutinin protein.					
SOURCE	Porphyromonas gingivalis.					
ORGANISM	Bacteria; Bacteroidetes; Bacteroides; Bacteroidales; Porphyromonadaceae; Porphyromonas.					
REFERENCE	1 (bases 1 to 1841)					
AUTHORS	Lepine, G. and Proquisle-Fox, A.					
TITLE	Duplication and differential expression of hemagglutinin genes in Porphyromonas gingivalis					
JOURNAL	Prokaryotobiol. Immunol. 11 (2), 65-78 (1996)					
MEDLINE	9304593					
PubMed	8941257					
REFERENCE	2 (bases 1 to 1841)					
AUTHORS	Lepine, G.					

JOURNAL	Theiss (1993) Oral Biology, University of Florida					
REFERENCE	3 (bases 1 to 1841)					
AUTHORS	Lepine, G.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-NOV-1993) Guylaine Lepine, Oral Biology, University of Florida, 1600 SW, Archer Road, Gainesville, Florida, 32610-0424.					
FEATURES	US					
location/Qualifiers	1..1841					
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-35_signal						
-10_signal						
gene						
CDS						
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/codon_start=1						
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Query Match						
Best Local Similarity						
Matches						
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RESULT 45						
LOCUS	AR049926/c		1841 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 5 from patent US 5824791.					
ACCESSION	AR049926					
VERSION	AR049926.1		GI:5971918			
KEYWORDS	US Patent 5,824,791					

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ORIGIN          /organism="unknown"
Query Match      9.9%; Score 18; DB 5; Length 1841;
Matched Similarity 10.9%; Positives 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1627 GCTGGAGAGCTCTTCGG 1610

Search completed: June 9, 2003, 12:33:20
Job time : 1271 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 08:36:50 ; Search time 474 Seconds
Database: us-09-550-163-1_copy_80_100
1289.365 Million cell updates/sec

Title: US-09-550-163-1_COPY_80_100

Perfect score: 21

Sequence: 1 attcttcacattccacag 21

Scoring table: IDENTITY_NUC

Gap: 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb.ba.*

2: gb.hg.*

3: gb.ro.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

7: gb.pl.*

8: gb.pr.*

9: gb.un.*

10: gb.vi.*

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12: en.fun.*

13: en.hum.*

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37: en.hum.*

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40: en.ov.*

41: en.pat.*

42: en.ph.*

43: en.pl.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	PB	ID	Description
1	21	100.0	732	6	AX406939	AX406939 Sequence
2	21	100.0	732	6	AX406941	AX406941 Sequence
3	21	100.0	732	6	AX406943	AX406943 Sequence
4	21	100.0	732	6	AX406945	AX406945 Sequence
5	21	100.0	732	9	AF071002	AF071002 Homo sapi
6	21	100.0	809	9	AF071002	AF071002 Homo sapi
7	21	100.0	24608	9	AF000320	AF000320 Homo sapi
8	21	100.0	10000	9	AF000320	AF000320 Homo sapi
9	21	100.0	10000	9	AF000320	AF000320 Homo sapi
10	21	100.0	10000	17	AF000120	AF000120 Homo sapi
11	21	100.0	340000	9	AP001719	AP001719 Homo sapi
12	20	95.2	99887	2	AC026481	AC026481 Homo sapi
13	19.4	92.4	732	6	AX406947	AX406947 Sequence
14	19.4	92.4	164456	2	AC078804	AC078804 Homo sapi
15	18.4	87.6	64677	2	AC079102	AC079102 Homo sapi
16	18.4	87.6	12444	2	AC091878	AC091878 Homo sapi
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18	18.4	87.6	152010	9	AC026785	AC026785 Homo sapi
19	18.4	87.6	157723	2	AC120989	AC120989 Oryza sat
20	18.4	87.6	171108	2	AC026504	AC026504 Homo sapi
21	18.4	87.6	180277	2	AC104270	AC104270 Oryza sat
22	18.4	87.6	193905	2	AC124440	AC124440 Mus muscu
23	18.4	87.6	228617	2	ALU73521	ALU73521 Mus muscu
24	18.4	87.6	228617	2	ALU73521	ALU73521 Mus muscu
25	18.4	87.6	228617	2	ALU73521	ALU73521 Mus muscu
26	18.4	87.6	318539	2	ALU77310	ALU77310 Mus muscu
27	17.8	84.8	37049	9	AC017026	AC017026 Homo sapi
28	17.8	84.8	37754	3	U23519	U23519 Caenorhabdi
29	17.8	84.8	69156	2	AC090542	AC090542 Homo sapi
30	17.8	84.8	69172	2	AC129960	AC129960 Bos tauru
31	17.8	84.8	89642	2	AC005136	AC005136 Homo sapi
32	17.8	84.8	89642	2	AC007958	AC007958 Genomic S
33	17.8	84.8	89642	2	AC007958	AC007958 Genomic S
34	17.8	84.8	95597	9	AC012555	AC012555 Homo sapi
35	17.8	84.8	107627	9	AL513218	AL513218 Human DNA
36	17.8	84.8	110000	2	AC009771	Continuation (2 of
37	17.8	84.8	110000	2	AC012386	Continuation (3 of
38	17.8	84.8	113693	9	HSDJIC16	AL049914 Human DNA
39	17.8	84.8	115863	9	HSDJIC16	AL049914 Human DNA
40	17.8	84.8	115863	9	HSDJIC16	AL049914 Human DNA
41	17.8	84.8	125415	9	HSDJIC16	AL049914 Human DNA
42	17.8	84.8	125415	9	AC026260	AC026260 Homo sapi
43	17.8	84.8	128294	9	AC073248	AC073248 Homo sapi
44	17.8	84.8	128461	9	AL390741	AL390741 Human DNA
45	17.8	84.8	134443	2	AC015547	AC015547 Homo sapi

ALIGNMENTS

RESULT 1	AX406939					
LOCUS	AX406939	732 bp	DNA	linear	PAT 14-JUN-2002	
DEFINITION	Sequence 1 from Patent WO0222875.					
ACCESSION	AX406939					
VERSION	AX406939.1	GI:21439814				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE 1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	Goldstein, S.A.					
Polymorphisms associated with cardiac arrhythmia						
Patent: WO 0222875-A 1 21-MAR-2002;						
JOURNAL						

Pred. No. is the number of results predicted by chance to have a

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source               Location/Qualifiers
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/db_xref="taxon:9606"
CDS
1..445
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amino acid 116"
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/db_xref="GI:21439815"
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NFYVILYLMWGMGFSFIIVALLVSTVSKRREHNDPHQVIVEDMGKYSQILN
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variation
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTTATCCAAATTCACAG 21
Db 80 ACTTATCCAAATTCACAG 100
RESULT 2
AX406941
LOCUS                732 bp DNA linear PAT 14-JUN-2002
DEFINITION           Sequence 3 from Patent WO0222875.
ACCESSION             AX406941
VERSION               AX406941.1 GI:21439816
KEYWORDS              human
ORGANISM              Homo sapiens
REFERENCE             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS               Goldstein.S.A.
TITLE                 Polymorphisms associated with cardiac arrhythmia
JOURNAL               Patent: WO 0222875-A 3 21-MAR-2002;
FEATURES              Location/Qualifiers
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/notes="mink-related peptide 1, wild type"
CDS
74..445
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/protein_id="CAD35180.1"
/db_xref="GI:21439817"
/translation="MSTLSNFTQLEDFRRIFITYMDNWRONTTAEALQAKVD
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LEESKATIHENIGAAGFKNP"
BASE COUNT          221 a 152 c 157 g 202 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 732;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTTATCCAAATTCACAG 21
Db 80 ACTTATCCAAATTCACAG 100
RESULT 3
AX406943
LOCUS                732 bp DNA linear PAT 14-JUN-2002
DEFINITION           Sequence 5 from Patent WO0222875.

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ACCESSION             AX406943
VERSION               AX406943.1 GI:21439818
KEYWORDS              human
ORGANISM              Homo sapiens
REFERENCE             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS               Goldstein.S.A.
TITLE                 Polymorphisms associated with cardiac arrhythmia
JOURNAL               Patent: WO 0222875-A 5 21-MAR-2002;
FEATURES              Location/Qualifiers
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/notes="mink-related peptide 1, Thr substituted for Met at
amino acid 54"
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LEESKATIHENIGAAGFKNP"
variation
/notes="The drug associated here was procainamide."
/replace="t"
BASE COUNT          221 a 153 c 157 g 201 t
ORIGIN
Query Match          100.0%; Score 21; DB 6; Length 732;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTTATCCAAATTCACAG 21
Db 80 ACTTATCCAAATTCACAG 100
RESULT 4
AX406945
LOCUS                732 bp DNA linear PAT 14-JUN-2002
DEFINITION           Sequence 7 from Patent WO0222875.
ACCESSION             AX406945
VERSION               AX406945.1 GI:21439820
KEYWORDS              human
ORGANISM              Homo sapiens
REFERENCE             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS               Goldstein.S.A.
TITLE                 Polymorphisms associated with cardiac arrhythmia
JOURNAL               Patent: WO 0222875-A 7 21-MAR-2002;
FEATURES              Location/Qualifiers
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amino acid 57"
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variation
/notes="The drug associated here was oxatamide."
/replace="t"
BASE COUNT          221 a 153 c 157 g 201 t

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 67;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTCCACAG 21
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Db 80 ACTTATCCAAATTTCCACAG 100

RESULT 5
AF071002      732 bp mRNA linear PRI 29-APR-1999
LOCUS Homo sapiens minK-related peptide 1 mRNA, complete cds.
DEFINITION AF071002
VERSION AF071002.1 GI:4704422
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 732)
AUTHORS Abbott.G.W., Gesti.F., Splawski.I., Buck.M.E., Lehmann.M.H.,
TITLE MIRP1 forms IKr potassium channels with HERG and is associated with
cardiac arrhythmia
JOURNAL Cell 97 (2), 175-187 (1999)
MEDLINE 99235979
PUBMED 10219239
REFERENCE 2 (bases 1 to 732)
AUTHORS Abbott.G.W., Gesti.F., Splawski.I., Buck.M.E. and Goldstein.S.A.N.
TITLE Submitted (05-JUN-1998) Section of Developmental Biology and
Biophysics, Department of Pediatrics and Boyer Center for Molecular
Medicine, Yale University School of Medicine, 295 Congress Avenue,
New Haven, CT 06536, USA
JOURNAL
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q11.1"
/tissue type="heart"
74..445
NOTE="potassium channel subunit; MIRP1"
/codon_start=1
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/db_xref="taxon:9606"
/db_xref="GI:4704423"
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LEESKATHIHGAGFMKSP"

BASE COUNT 221 a 152 c 157 g 202 t
ORIGIN
Query Match      100.0%; Score 21; DB 9; Length 732;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTCCACAG 21
|||||
Db 80 ACTTATCCAAATTTCCACAG 100

RESULT 6
AF302095      809 bp mRNA linear PRI 14-SEP-2000
LOCUS Homo sapiens voltage-gated K+ channel subunit MIRP1 (KCNE2) mRNA,
complete cds.
DEFINITION AF302095
VERSION AF302095.1 GI:10121887
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 809)
AUTHORS Domenech.A., Estivill.X. and de la Luna.S.
TITLE Cloning of human MIRP1 cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 809)
AUTHORS Domenech.A., Estivill.X. and de la Luna.S.
TITLE Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
Institut Recerca Oncologica, Avia. de Castelldefels Km 2.7,
L'Hospitalet de Llobregat, Barcelona 08907, Spain
JOURNAL
FEATURES
source Location/Qualifiers
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/chromosome="21"
/map="21q22"
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141..512
CODON_START=1
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LEESKATHIHGAGFMKSP"

BASE COUNT 247 a 172 c 189 g 200 t 1 others
ORIGIN
Query Match      100.0%; Score 21; DB 9; Length 809;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTCCACAG 21
|||||
Db 147 ACTTATCCAAATTTCCACAG 167

RESULT 7
AP000320      24608 bp DNA linear PRI 20-NOV-1999
LOCUS Homo sapiens genomic DNA, chromosome 21q22.1, D12S26-AML region,
clone:Q12C8, complete sequence.
DEFINITION AP000320
VERSION AP000320.1 GI:4835689
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:Q12C8.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 24608)
AUTHORS Fukui.A., Yada.T., Totoki.Y. and Sakaki.Y.
TITLE Published Only in DataBase (1999)
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 24608)
AUTHORS Hattori.M., Ishii.K., Toyoda.A., Taylor.T.D., Hong-Seog.P.,
Fujiyama.A., Yada.T., Totoki.Y. and Sakaki.Y.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1999) Mashima Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genes and Environment Research Center,
Kiwakato Univ. 1-15-1 Kiwakato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@icr.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
COMMENT The sequence is a part of the data (ACCESSION No. AP000165 -
AP000173).
The sequencing project is supported by Japan Science Technology

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Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).

FEATURES

source
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ORIGIN

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DB 15702 ACTTATCCAAATTCACAG 15722

RESULT 9

AP000052

LOCUS

DEFINITION Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens DNA, clone:245P17-f4A4f_2.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1998)
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Direct Submission
Submitted (11-MAY-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgsc.ims.u-tokyo.ac.jp, Tel:0427-78-9312, Fax:0427-78-9561)
Lab. sequence is produced by Kitasato University JST sequencing Principal Investigator: Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax: +81-3-5449-5445, sakaki@hgsc.ims.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by Human Genome Sequencing in ALIS project of JST
Japan Science and Technology Corporation (JST)
Chiyoda-ku, Chiba-shi, Tokyo 105-0038, Japan
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (<http://www.alis.tokyo.jst.go.jp/HGS/top.html>) or send email to webmaster@www.nlis.tokyo.jst.go.jp.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="245P17-f4A4f_2"

FEATURES

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BASE COUNT 27603 a 21934 c 22513 g 27950 t
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Best Local Similarity 100.0%; Pred. No. 19; Indels 0; Gaps 0; Matches 21; Conservative 0; Mismatches 0;

QY 1 ACTTATCCAAATTCACAG 21

DB 80224 ACTTATCCAAATTCACAG 80244

RESULT 9

AP000167

LOCUS

DEFINITION Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AMU clone B3344P14-f5028, segment 3/9, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

DB

RESULT 10

AP000120

LOCUS

AC

AP000120;

SV

AP000120.1

DT

26-SEP-1999

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Buguelskiy L., Bonhgalter B., Brown A., Burkett G., Collins S.,
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 Howard-Pierre N., Grant G., Hagos B., Headford A., Horton L.,
 Howland J.C., Iliev I., Johnson R., Jones C., Kann L., Karataa A.,
 Klein J., Labouque K., Lamazares R., Landers T., Lebecky J.,
 McArthur M., McEwan P., McGuire K., McKernan K., McPherson R.,
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 O'Neil D., Olivier T.M., Oliver J.C., Peterson K., Riegler N.,
 Pisanic C., Pollara V., Raymond C., Riley R., Rogov P., Rothman D.,
 Santos R., Schauer S., Severi P., Spencer B.,
 Stange-Thumm N., Stojanovic N., Subramanian A., Talamas J.,
 Vassiliou H., Vignat B., Voisard M., Weaver M., Trigglio J.,
 Young G., Zainoun J., Zimmer A. and Zody M.
 Direct Submission
 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 30, 2000 this sequence version replaced gi:7280305.
 All repeats were identified using RepeatMasker:
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center -----
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Project name: 13_2
 Center name: 2_1_B_3

 * NOTE: This record contains 122 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying contigs that may have been missed by
 * overlap relationships among clones to be added.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.
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 * 2 877: gap of 100 bp
 * 3 877: gap of 100 bp
 * 4 1629 1728: gap of 100 bp in length
 * 5 1729 2488: contig of 760 bp in length
 * 6 2489 2588: gap of 100 bp
 * 7 2589 3356: contig of 768 bp in length
 * 8 3357 3456: gap of 100 bp
 * 9 3457 4204: contig of 748 bp in length
 * 10 4205 4304: gap of 100 bp
 * 11 4305 5161: contig of 857 bp in length
 * 12 5162 5161: contig of 100 bp
 * 13 5162 5161: contig of 765 bp in length
 * 14 5928 6027: gap of 100 bp
 * 15 6028 6788: contig of 761 bp in length
 * 16 6789 6888: gap of 100 bp
 * 17 6889 7666: contig of 778 bp in length
 * 18 7667 7766: gap of 100 bp
 * 19 7767 8553: gap of 100 bp
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 * 22 9435 9534: gap of 100 bp
 * 23 9535 10302: contig of 768 bp in length
 * 24 10303 10402: gap of 100 bp
 * 25 10403 11153: contig of 751 bp in length
 * 26 11154 11253: gap of 100 bp
 * 27 11254 12005: contig of 752 bp in length
 * 28 12006 12105: gap of 100 bp
 * 29 12106 12189: contig of 774 bp in length
 * 30 12880 12978: gap of 100 bp in length
 * 31 12980 13755: contig of 776 bp in length
 * 32 13756 13855: gap of 100 bp
 * 33 13856 14624: contig of 769 bp in length
 * 34 14625 14724: gap of 100 bp
 * 35 14725 15417: contig of 631 bp in length
 * 36 15418 15500: gap of 100 bp
 * 37 15501 16265: contig of 748 bp in length
 * 38 16266 16365: gap of 100 bp
 * 39 16366 17122: contig of 757 bp in length
 * 40 17123 17222: gap of 100 bp
 * 41 17223 17986: contig of 764 bp in length
 * 42 17987 18086: gap of 100 bp
 * 43 18087 18850: contig of 784 bp in length
 * 44 18851 19713: gap of 100 bp
 * 45 19714 19813: gap of 100 bp
 * 46 19814 20587: contig of 774 bp in length
 * 47 20588 20687: gap of 100 bp
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 * 49 21465 21564: gap of 100 bp
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 * 51 22432 22431: gap of 100 bp
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 * 54 23301 24056: contig of 766 bp in length
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 * 57 24928 25027: gap of 100 bp
 * 58 25028 25795: contig of 788 bp in length
 * 59 25796 25926: gap of 100 bp
 * 60 25927 26768: gap of 100 bp
 * 61 26769 27532: contig of 764 bp in length
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 * 64 28406 28505: gap of 100 bp
 * 65 28506 28248: contig of 743 bp in length
 * 66 28507 29314: gap of 100 bp
 * 67 29315 30114: contig of 766 bp in length
 * 68 30115 30214: gap of 100 bp
 * 69 30215 30983: contig of 769 bp in length
 * 70 30984 31083: gap of 100 bp
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 * 73 31941 32700: contig of 780 bp in length
 * 74 32701 32800: gap of 100 bp
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 * 81 35351 36118: contig of 788 bp in length
 * 82 36119 36218: gap of 100 bp
 * 83 36219 37061: contig of 793 bp in length
 * 84 37062 37822: contig of 761 bp in length
 * 85 37823 37922: gap of 100 bp
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 * 87 38678 38777: gap of 100 bp
 * 88 38778 39541: contig of 784 bp in length
 * 89 39542 39641: gap of 100 bp
 * 90 39642 40383: contig of 742 bp in length
 * 91 40384 40483: gap of 100 bp
 * 92 40484 41257: contig of 774 bp in length
 * 93 41258 41357: gap of 100 bp
 * 94 41358 42118: contig of 761 bp in length
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 * 96 42219 42917: contig of 699 bp in length
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TITLE
JOURNAL

COMMENT


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JOURNAL
REFERENCE 2 (Unpublished
AUTHORS Worley K.C.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 164456)
AUTHORS Worley K.C.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jun 17, 2002 this sequence version replaced gi:20335729.
----- Genome Center
Center: Baylor College of Medicine
Contact: hgsc@bcm.tmc.edu
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HFTN
Center clone name: RP11-489M17
----- Summary Statistics
Sequencing Sector: ML/Rediply: 75% of reads
Chemistry: Dye-terminator Big Dye, version 0.950139
Assembly program: Phrap, version 0.950139
Consensus quality: 158577 bases at least Q40
Consensus quality: 160839 bases at least Q30
Consensus quality: 161950 bases at least Q20
Estimated insert size: 165132; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/GenbankDraftData.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
hyphens. The size of the gaps is unknown.
This record will be updated with the sequence as soon
as soon as it is available and the accession number will
be preserved.
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7695 7794: gap of unknown length
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31130 31140: gap of unknown length
31140 52112: contig of 20873 bp in length
52112 52113: gap of unknown length
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78976 79075: gap of unknown length
79075 118007: contig of 38932 bp in length
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118108 Location/Qualifiers
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BASE COUNT 52500 a 30465 c 29464 g 50085 t 1942 others
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Best Local Similarity 95.24; Pred. No. 82;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ACTTATTCACATTTTCACAG 21
Db 117667 ACTTATTCACATTTTCACATG 117687

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RESULT 15
AC079102/c
LOCUS Homo sapiens chromosome 4 clone RP11-113B map 4, LOW-PASS SEQUENCE
DEFINITION SAMPLING.
AC079102
VERSION 1.0
KEYWORDS LOW-PASS.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 64677)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Nature
COMMENT Homo sapiens chromosome 4, clone RP11-113B
2 (bases 1 to 64677)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Batra,N., Bustien,V., Bada,F., Boguslavsky,L.,
Boukigalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chepeil,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeRellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhugh,M., Gage,D., Galagan,W., Gage,D., Gindoff,S., Goyette,M.,
Hahn,L., Grand-Prere,M., Hager,B., Hendrick,A., Horton,L.,
Lander,E., Johnson,R., Jones,A., Jones,C., Jones,K.,
Lamasara,P., Lander,T., Lechoczky,J., Levine,R., Liu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheters,R., Meldrim,J., Meneses,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pignatelli,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogers,J., Rong,S., Rong,Y., Saito,N., Schaefer,A., Schaefer,N.,
Sodergren,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strausz,N., Subramanian,A., Talanas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Traversan,M., Trigilio,J., Vassiliev,H., Viel,R., Vo.A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (18-AUG-2000) Whitehead Institute/MIT Center for Genome
Research, 77 Avenue Louis Pasteur, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WMR
Web site: http://www.seg.wi.mit.edu
----- Project Information
Center project name: L10750
Center clone name: L13_B_8
NOTE: This record contains 79 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
from the contigs. This record is not suitable for
arbitrary low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allow
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
738: contig of 738 bp in length
739 838: gap of 100 bp
839 1599: Contig of 751 bp in length
1599 1689: gap of 100 bp
1690 2424: contig of 735 bp in length
2425 2524: gap of 100 bp
2525 3230: contig of 706 bp in length
3231 3330: gap of 100 bp

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3331 4051: contig of 721 bp in length
4052 4151: gap of 100 bp
4152 4859: contig of 708 bp in length
4860 4959: gap of 100 bp
4960 5783: contig of 774 bp in length
5784 6581: contig of 718 bp in length
6582 6601: gap of 100 bp
6602 7334: contig of 713 bp in length
7335 7434: gap of 100 bp
7435 8144: contig of 710 bp in length
8145 8244: gap of 100 bp
8245 8950: contig of 706 bp in length
8951 9050: gap of 100 bp
9051 9756: contig of 706 bp in length
9757 9856: gap of 100 bp
9857 10567: contig of 711 bp in length
10568 10667: gap of 100 bp
10668 11384: contig of 717 bp in length
11385 11484: gap of 100 bp
11485 12272: contig of 781 bp in length
12273 12981: contig of 706 bp in length
12982 13081: gap of 100 bp
13082 13796: contig of 715 bp in length
13797 13896: gap of 100 bp
13897 14617: contig of 721 bp in length
14618 14717: gap of 100 bp
14718 15471: contig of 755 bp in length
15472 15531: gap of 100 bp
15532 16247: contig of 710 bp in length
16248 16347: gap of 100 bp
16348 17082: contig of 735 bp in length
17083 17182: gap of 100 bp
17183 17917: contig of 735 bp in length
17918 18017: gap of 100 bp
18018 18442: contig of 725 bp in length
18443 18842: gap of 100 bp
18843 19541: contig of 699 bp in length
19542 19641: gap of 100 bp
19642 20355: contig of 714 bp in length
20356 20455: gap of 100 bp
20456 212186: contig of 711 bp in length
21219 21596: gap of 100 bp
21597 22083: contig of 697 bp in length
22084 22806: contig of 723 bp in length
22807 22906: gap of 100 bp
22907 23625: contig of 719 bp in length
23626 23725: gap of 100 bp
23726 24463: contig of 738 bp in length
24464 25297: contig of 734 bp in length
25298 25397: gap of 100 bp
25398 26110: contig of 713 bp in length
26111 26210: gap of 100 bp
26211 26924: contig of 714 bp in length
26925 27024: gap of 100 bp
27025 27731: contig of 707 bp in length
27732 28552: contig of 721 bp in length
28553 28652: gap of 100 bp
28653 29164: contig of 712 bp in length
29165 29464: gap of 100 bp
29465 30201: contig of 737 bp in length
30202 30301: gap of 100 bp
30302 31150: contig of 749 bp in length
31151 31847: contig of 697 bp in length
31848 31947: gap of 100 bp
31948 32684: contig of 737 bp in length
32685 32784: gap of 100 bp
32785 33511: contig of 727 bp in length

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33512 33611: gap of 100 bp
33612 34355: contig of 744 bp in length
34356 34455: gap of 100 bp
34456 35167: contig of 712 bp in length
35168 35859: gap of 100 bp
35860 35973: contig of 706 bp in length
35974 36073: gap of 100 bp
36074 36795: contig of 722 bp in length
36796 36895: gap of 100 bp
36896 37594: contig of 699 bp in length
37595 37694: gap of 100 bp
37695 38402: contig of 708 bp in length
38403 38502: gap of 100 bp
38503 39233: contig of 730 bp in length
39233 39332: gap of 100 bp
39333 40054: contig of 722 bp in length
40055 40154: gap of 100 bp
40155 40904: contig of 750 bp in length
40905 41004: gap of 100 bp
41005 41741: contig of 703 bp in length
41742 42566: contig of 723 bp in length
42565 42664: gap of 100 bp
42665 43383: contig of 719 bp in length
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43484 44197: contig of 714 bp in length
44198 44297: gap of 100 bp
44298 44997: contig of 700 bp in length
44999 45098: gap of 100 bp
45098 45798: contig of 701 bp in length
45799 45898: gap of 100 bp
45899 46636: contig of 738 bp in length
46637 46736: gap of 100 bp
46737 47423: contig of 687 bp in length
47424 47523: gap of 100 bp
47524 48364: contig of 710 bp in length
48365 48364: gap of 100 bp
48365 49092: contig of 728 bp in length
49093 49192: gap of 100 bp
49193 49821: contig of 729 bp in length
49822 50021: gap of 100 bp
50022 50749: contig of 728 bp in length
50750 50849: gap of 100 bp
50850 51661: contig of 711 bp in length
51662 51661: gap of 100 bp
51662 52375: contig of 714 bp in length
52376 52475: gap of 100 bp
52476 53198: contig of 723 bp in length
53199 53298: gap of 100 bp
53299 54016: contig of 718 bp in length
54017 54152: gap of 100 bp
54117 54152: gap of 100 bp
54825 54924: gap of 100 bp
54925 55651: contig of 727 bp in length
55652 55751: gap of 100 bp
55752 56460: contig of 709 bp in length
56461 56560: gap of 100 bp
56561 57299: contig of 739 bp in length

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Query Match      87.68;  Score 18.4;  DB 2;  Length 64677;
Best Local Similarity 95.04;  Pred. No. 2.8e+02;
Matches 19;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1  ACTTATCCAAATTCACACA 20
Db      49052 ACATATCCAAATTCACACA 49033

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Search completed: June 9, 2003, 09:09:53
Job time : 619 secs

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XX WPI; 2001-488901/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells -
 XX Claim 25; SEQ ID No 14365; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 XX (SENP). The present sequence is one such probe. The SENPs are derived
 XX from human Hela cells. The SENPs can be used to produce a single exon
 XX microarray, which can be used for measuring human gene expression in a
 XX sample derived from human cervical epithelial cells. By measuring gene
 XX expression, the probes are therefore useful in grading and/or staging
 XX cervical cancer. The probes are therefore useful in the treatment of
 XX cervical cancer.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 22; Length 372;
 XX Best Local Similarity 100.0%; Pred. No. 6.1;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTTATCCAATTTCCACAG 21
 DB 7 ACTTTATCCAATTTCCACAG 27
 RESULT 2
 ID AAI09965 standard; DNA; 372 BP.
 XX AC AAS00245;
 XX 10-MAY-2001 (first entry)
 XX Homo sapiens.
 DE Probe #9556 used to measure gene expression in human breast sample.
 XX Probe; human; breast disease; breast cancer; development disorder; as;
 XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX Homo sapiens.
 XX WO200157270-A2.
 XX 09-AUG-2001.
 XX 29-JAN-2001; 2001WO-US00661.
 XX 04-FEB-2000; 2000US-0160312.
 XX 24-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000US-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-476286/51.
 XX Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -
 XX Claim 25; SEQ ID No 9556; 32pp; English.
 XX The present invention relates to novel single exon nucleic acid probes.
 XX The present sequence is one such probe. The probes are useful for
 XX measuring human gene expression in a human breast sample, where the probe

CC hybridises at high stringency to a nucleic acid expressed in the human
 CC breast. The probes are useful for predicting, diagnosing, grading,
 CC staging, monitoring and prognosing diseases of the human breast,
 CC particularly those diseases with polygenic aetiology. The diseases
 CC include: breast cancer, disorders of development, inflammatory diseases
 CC of the breast, benign tumours, hyperplastic changes, proliferative breast disease and
 CC non-neoplastic tumours.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 22; Length 372;
 XX Best Local Similarity 100.0%; Pred. No. 6.1;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTTATCCAATTTCCACAG 21
 DB 7 ACTTTATCCAATTTCCACAG 27
 RESULT 3
 ID AAS00245 standard; DNA; 372 BP.
 XX AC AAS00245;
 XX 10-MAY-2001 (first entry)
 XX Homo sapiens.
 DE Human potassium channel regulatory protein, Mink2, DNA sequence.
 XX Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
 XX angina; asthma; diabetes; renal ineffecticiency; urinary incontinence;
 XX irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..372
 XX FT /*tag= a
 XX /product= "MINK2 potassium channel protein"
 XX WO200114403-A1.
 XX 01-MAR-2001.
 XX 18-AUG-2000; 2000WO-US22799.
 XX 20-AUG-1999; 99US-0379201.
 XX (UYCA-) UNIV CASE WESTERN RESERVE.
 XX Ficker E, Wible B, Brown AW;
 XX WPI; 2001-218424/22.
 XX P-PSDB; AAU00215.
 XX Novel potassium channel gene termed Mink2 encoding potassium channel
 XX regulatory protein useful for screening compounds that are useful for
 XX treating diseases caused by aberrant potassium activity -
 XX Claim 1; Fig 9; 35pp; English.
 XX The sequence represents the coding sequence of human potassium channel
 XX regulatory protein, Mink2. Mink2 sequence is useful for producing a
 XX recombinant protein. The protein is useful for screening compounds for
 XX screening of agonistic or antagonistic compounds that are useful for
 XX treating diseases caused by aberrant potassium activity, such as human
 XX cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal
 XX insufficiency, urinary incontinence, irritable colon, epilepsy,
 XX cerebrovascular ischaemia, and autoimmune disease.

SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
Query Match 100.0%; Score 21; DB 22; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
Db 7 ACTTATCCAAATTTTCACAG 27

RESULT 4
ABA44797

ID ABA44797 standard; DNA; 450 BP.
AC ABA44797;
XX ABA44797;
DT 01-FEB-2002 (first entry)
DE Human breast cell single exon nucleic acid probe #3492.
XX Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer; ss.
XX Homo sapiens.
XX WO200157271-A2.
PN 09-AUG-2001.
PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00662.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 21-SEP-2000; 2000US-0234697.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
FI WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
XX useful for measuring gene expression in sample derived from human
XX breast, comprises number of single exon nucleic acid probes -
XX Claim 1; SEQ ID NO 3492; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and Br 474 cells. The method involves contacting
XX the probes with a collection of detectably labelled nucleic acids
XX derived from mRNA of human breast, and then measuring the label
XX by means of a microarray. The method is suitable for the rapid
XX verification of the expression of regions of genomic DNA predicted to
XX encode proteins. They are useful for gene discovery, and for
XX determining predisposition and/or prognosing breast disease. Gene
XX expression analysis is useful for assessing the toxicity of chemical
XX agents on cells. The microarray of this invention presents a far greater
XX diversity of probes for measuring gene expression, with far less bias
XX than sequence tag microarrays. The method is suitable for the
XX rapid identification of genes that are up-regulated or down-regulated.
XX The present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
Db 162 ACTTATCCAAATTTTCACAG 182

RESULT 5
ABA55252

ID ABA55252 standard; DNA; 450 BP.
AC ABA55252;
XX ABA55252;
DT 01-FEB-2002 (first entry)
DE Human foetal liver single exon nucleic acid probe #3557.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
PN 09-AUG-2001.
PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00669.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 21-SEP-2000; 2000US-0234697.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
FI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver -
XX Claim 1; SEQ ID NO 3557; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
Db 162 ACTTATCCAAATTTTCACAG 182

RESULT 6
ABA24997

ID ABA24997 standard; DNA; 450 BP.
AC ABA24997;
XX ABA24997;
DT 01-FEB-2002 (first entry)
DE Human foetal liver single exon nucleic acid probe #3557.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
PN 09-AUG-2001.
PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00669.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 21-SEP-2000; 2000US-0234697.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
FI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver -
XX Claim 1; SEQ ID NO 3557; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
Db 162 ACTTATCCAAATTTTCACAG 182

RESULT 6
ABA24997

ID ABA24997 standard; DNA; 450 BP.
AC ABA24997;
XX ABA24997;
DT 01-FEB-2002 (first entry)
DE Human foetal liver single exon nucleic acid probe #3557.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
PN 09-AUG-2001.
PD 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00669.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 21-SEP-2000; 2000US-0234697.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
FI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver -
XX Claim 1; SEQ ID NO 3557; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

AC ABA24597;
 XX 23-JAN-2002 (first entry)
 DE Probe #3463 for gene expression analysis in human heart cell sample.
 XX Human, gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease; ss.
 XX Homo sapiens.
 XX WO200157274-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00666.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0609408.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX Claim 1; SEQ ID No 3463; 530pp; English.
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging, and
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC including heart disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/whdnet/pct_sequences.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 22; Length 450;
 XX Best Local Similarity 100.0%; Pred. No. 6.1;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTATTCCAATTCACACAG 21
 Db 162 ACTTATTCCAATTCACACAG 182
 RESULT 7
 AAK03508
 ID AAK03508 standard; DNA; 450 BP.
 XX AAK03508;
 XX 05-NOV-2001 (first entry)
 XX Human brain expressed single exon probn SEQ ID NO: 3499.
 DE Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsay; cancer; ss.
 XX Homo sapiens.
 XX WO200157275-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00667.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0609408.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX Example 4; SEQ ID NO: 3499; 650pp + Sequence Listing; English.
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancer. The present sequence is one of the probes of the
 CC invention.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 22; Length 450;
 XX Best Local Similarity 100.0%; Pred. No. 6.1;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACTTATTCCAATTCACACAG 21
 Db 162 ACTTATTCCAATTCACACAG 182
 RESULT 8
 AAK28962
 ID AAK28962 standard; DNA; 450 BP.
 XX AAK28962;
 XX 06-NOV-2001 (first entry)
 XX Human bone marrow expressed single exon probe SEQ ID NO: 3519.
 DE Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 XX WO200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0609408.
 XX 03-AUG-2000; 2000US-0632366.

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PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0234689.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX Example 4; SEQ ID NO: 3519; 658pp + sequence listing; English.
XX The present invention provides a number of single exon nucleic acid
CC and gene sequences expressed in the human
CC bone marrow. They can be used in the diagnosis of
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
XX Query Match 100.0%; Score 21; DB 22; Length 450;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTTATCAATTTCACACAG 21
Db 162 ACTTATCAATTTCACACAG 182
RESULT 9
AA113549
ID AA113549 standard; DNA; 450 BP.
AC AA113549;
XX 12-OCT-2001 (first entry)
XX Probe #3482 for gene expression analysis in human cervical cell sample.
DE Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX Homo sapiens.
XX WO200157278-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00670.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX Claim 25; SEQ ID No 3482; 487pp; English.

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CC The present invention relates to human single exon nucleic acid probes
CC (SNP) derived from one such probe. The SNPs are derived
CC from human cells. The SNPs are used in a probe
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published\_pat\_sequences.
XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
XX Query Match 100.0%; Score 21; DB 22; Length 450;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACTTATCAATTTCACACAG 21
Db 162 ACTTATCAATTTCACACAG 182
RESULT 10
AA134911
ID AA134911 standard; DNA; 450 BP.
XX 30-JAN-2001; 2001WO-US00663.
XX 09-AUG-2001.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 01-AUG-2000; 2000US-0623266.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488997/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 25; SEQ ID No 3597; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SNP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
XX Query Match 100.0%; Score 21; DB 22; Length 450;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ACTTATCCATTTTCACAG 21
DB 162 ACTTATCCATTTTCACAG 182

RESULT 11
ID AAI03438
XX AAI03438 standard; DNA, 450 BP.
AC AAI03438;
XX 09-OCT-2001 (first entry)
DT Probe #3429 used to measure gene expression in human breast sample.
DE Probe, human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX Homo sapiens.
OS WO200157270-A2.
XX 09-AUG-2001.
PD 29-JAN-2001; 2001WO-US00661.
XX 04-FEB-2000; 2000US-0180112.
PR 26-MAY-2000; 2000US-207456P.
XX 03-JUN-2000; 2000US-0204406.
PR 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PT WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX Claim 25; SEQ ID No 3429; 322pp; English.
XX The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridizes at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC screening, monitoring and prognosticating diseases of the human breast,
CC including epithelial, connective tissue, and hematopoietic diseases.
CC include: breast cancer; disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published/pct_sequences.
SQ Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTTATCCATTTTCACAG 21
DB 162 ACTTATCCATTTTCACAG 182

RESULT 12
ABS03496

ABS03496 standard; DNA; 450 BP.
XX ABS03496;
AC 19-AUG-2002 (first entry)
XX Human genome-derived single exon probe from lung SEQ ID No 3487.
DT Human;
DE Human; de; single exon probe; asthma; lung cancer; COPD; I10;
KW chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Heremans-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
XX pulmonary alveolar proteinosis; pulmonary alveolar micromatosis;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX Homo sapiens.
OS WO200186003-A2.
XX 15-NOV-2001.
PD 30-JAN-2001; 2001WO-US00665.
XX 04-FEB-2000; 2000US-180112P.
PR 26-MAY-2000; 2000US-207456P.
XX 03-JUN-2000; 2000US-0204406.
PR 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PT WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX Claim 1; SEQ ID No 3487; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12887 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of a
XX nucleic acid expressed in the human lung, measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of the probe
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarray having a probe with the exon, where a common pattern of
XX expression is observed across the microarray, the exon is identified that
XX the probe should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene
XX expression analysis, and for identifying exons in a gene, particularly
XX using human lung derived mRNA and for the study of lung diseases
XX such as asthma, lung cancer, chronic obstructive pulmonary disease

CC (COPD): interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, emphysema, chronic bronchitis, chronic obstructive pulmonary
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a single exon
 CC probe of the invention. for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 450;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ACTTATTCGAATTCACAC 21
 DB 162 ACTTATTCGAATTCACAC 182
 RESULT 13
 AA115256
 ID AA115256 standard; DNA; 471 BP.
 AC AA115256;
 XX AA115256;
 XX 12-OCT-2001 (first entry)
 DT Probe H5189 for gene expression analysis in human cervical cell sample.
 DE Probe: human; microarray; gene expression; cervical epithelial cell;
 XX cervical cancer; es.
 XX Homo sapiens.
 XX WO200157278-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00670.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI, 2001-488901/53.
 DR Novel single exon nucleic acid probe used for
 XX analyzing gene expression in human cervical epithelial cells -
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX Claim 25; SEQ ID No 5189; 487pp; English.
 XX The present invention relates to human single exon nucleic acid probes
 XX (SENPs). The present sequence is one such probe. The SENPs are derived
 XX from human HeLa cells. The SENPs can be used to produce a single exon
 XX microarray, which can be used for measuring human gene expression in a
 XX sample derived from human cervical epithelial cells. By measuring gene
 XX expression, the probes are therefore useful in grading and/or staging
 XX of diseases of the cervix, notably cervical cancer.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
 CC Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
 SQ Query Match 100.0%; Score 21; DB 22; Length 471;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ACTTATTCGAATTCACAC 21
 DB 245 ACTTATTCGAATTCACAC 265
 RESULT 14
 AA104990
 ID AA104990 standard; DNA; 471 BP.
 AC AA104990;
 XX AA104990;
 XX 09-OCT-2001 (first entry)
 DT Probe #4981 used to measure gene expression in human breast sample.
 DE Probe: human; breast disease; breast cancer; development disorder; es;
 XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX Homo sapiens.
 XX WO200157270-A2.
 XX 09-AUG-2001.
 XX 29-JAN-2001; 2001WO-US00661.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0623666.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI, 2001-476286/51.
 DR Novel single exon nucleic acid probe used to measuring gene expression
 XX in a human breast -
 PT Claim 25; SEQ ID No 4981; 322pp; English.
 XX The present invention relates to novel single exon nucleic acid probes.
 XX The present sequence is one such probe. The probes are useful for
 XX measuring human gene expression in a human breast sample, where the probe
 XX hybridizes at high stringency to a nucleic acid expressed in the human
 XX breast. The probes are useful for measuring gene expression in the human
 XX breast, staging, monitoring and proposing diseases of the human breast,
 XX particularly those diseases with polygenic aetiology. The diseases
 XX include: breast cancer, disorders of development, inflammatory diseases
 XX of the breast, fibrocystic changes, proliferative breast disease and
 XX non-carcinoma tumours.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
 SQ Query Match 100.0%; Score 21; DB 22; Length 471;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTTATCCAAATTCACAG 21
DB 245 ACTTATCCAAATTCACAG 265

RESULT 15

AAF80269

ID AAF80269 standard; DNA: 471 BP.

XX

AC AAF80269;

DT 29-JUN-2001 (first entry)

XX

XX Nucleotide sequence of human potassium channel subunit Isk2.

XX

KW Human; potassium channel; Isk2; gene therapy; gastric motility;

KW gastric acid secretion; anti-arrhythmic agent; myocardial infarction; as.

XX

OS Homo sapiens.

XX

XX Key

FT 79-150

FT CDS

FT /tag= a

FT /product= "potassium channel subunit Isk2"

XX

PN WO200127246-A1.

XX

XX 19-APR-2001.

XX

PF 10-OCT-2000; 2000WO-US28014.

XX

PR 12-OCT-1999; 99US-0158781.

XX

PA (MERI) MERCK & CO INC.

XX

XX Swanson RJ, Liu Y, Folander K;

XX

WI WPI: 2001-273764/28.

DR P-PSDB; AAB67800.

XX

PT New DNA encoding the Isk2 potassium channel subunit, useful e.g. for

PT detecting mutations and screening for therapeutic agents -

XX

XX Claim 3; Fig 1A; 45pp; English.

XX

CC The present sequence encodes a human potassium channel subunit,

CC designated Isk2. The Isk2 polynucleotide, and derived probes, are

CC used diagnostically to detect mutations in the Isk2 gene, to determine

CC levels of mRNA expression and to isolate homologous sequences; for

CC recombinant expression of Isk2; in gene therapy to increase potassium

CC channel activity and to generate transgenic animals; as models and

CC for studying the mechanism of action of drugs that affect gastric motility and

CC activity of Isk2 and in the treatment of gastric motility and

CC gastric acid secretion; and to raise specific antibodies. Isk2

CC modulators are potentially useful for treating diseases associated with

CC increased or reduced potassium channel activity, e.g. as

CC anti-arrhythmic agents for treating myocardial infarction and as

CC regulators of gastric acid secretion.

XX

XX Sequence 471 BP; 143 A; 110 C; 103 G; 115 T; 0 other;

XX

Query Match 100.0%; Score 21; DB 22; Length 471;

Best Local Similarity 100.0%; Pred. No. 6.1;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTTATCCAAATTCACAG 21

DB 85 ACTTATCCAAATTCACAG 105

Search completed: June 9, 2003, 08:51:24

Job time : 121 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 08:36:51 | Search time 31.5 seconds

(Without alignments)
204,431 Million cell updates/sec

Title: US-09-550-163-1_COPY_80_100

Perfect score: 21

Sequence: 1 acttatccaattccacag 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/pdata/1/ina/backfiles1.seq.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.4	78.1	6402	2	US-08-670-707A-36
C 2	16.4	78.1	6402	4	US-09-037-601-36
C 3	16.4	78.1	6402	6	US-09-037-601-36
C 4	15.8	75.2	627	4	US-09-532-658-39
C 5	15.8	75.2	627	4	US-08-962-281-1
C 6	15.8	75.2	1211	4	US-09-198-603C-25
C 7	15.8	75.2	5000	3	US-09-147-522-5
C 8	15.4	73.3	2244	4	US-08-203-532F-1
C 9	15.4	73.3	2244	4	US-09-078-465-1
C 10	15.4	73.3	2244	5	PTC-US95-01882A-1
C 11	15.4	73.3	2430	4	US-08-945-258-40
C 12	15.4	73.3	2430	4	US-08-945-258-40
C 13	15.4	73.3	2430	4	US-08-990-571-3
C 14	15.4	73.3	2430	4	US-08-990-571-40
C 15	15.4	73.3	2430	4	US-08-723-142A-3
C 16	15.4	73.3	2430	4	US-08-723-142A-40
C 17	15.4	73.3	2430	4	US-09-528-784A-3
C 18	15.4	73.3	2430	4	US-09-528-784A-40
C 19	15.4	73.3	2430	4	US-09-528-784A-206
C 20	15.4	73.3	45325	4	US-09-433-702B-206
C 21	15.2	72.4	865	4	US-09-280-116-63
C 22	15.2	72.4	865	4	US-09-796-110-1
C 23	15.2	72.4	1001	4	US-09-641-638-441
C 24	15.2	72.4	1001	4	US-09-641-638-450
C 25	15.2	72.4	1622	4	US-09-004-393B-1
C 26	15.2	72.4	1713	4	US-08-759-436-1
C 27	15.2	72.4	2706	2	US-08-670-707A-61

C 28	15.2	72.4	2706	2	US-09-005-069-61
C 29	15.2	72.4	2706	2	US-09-005-069-61
C 30	15.2	72.4	4626	2	US-08-484-859-20
C 31	15.2	72.4	4626	2	US-08-484-859-20
C 32	15.2	72.4	4670	3	US-08-717-284-41
C 33	15.2	72.4	4670	3	US-08-717-284-41
C 34	15.2	72.4	4999	4	US-09-470-618-14
C 35	15.2	72.4	4999	4	US-09-470-618-14
C 36	15.2	72.4	5035	2	US-09-364-862-14
C 37	15.2	72.4	5035	2	US-08-882-083-1
C 38	15.2	72.4	5035	2	US-08-558-107-1
C 39	15.2	72.4	5035	2	US-08-558-107-1
C 40	15.2	72.4	7056	1	US-09-242-539-1
C 41	15.2	72.4	7056	1	US-09-242-539-1
C 42	15.2	72.4	8241	6	US-08-121-202-1
C 43	15.2	72.4	8241	6	5171844-1
C 44	15.2	72.4	8967	1	US-08-366-851A-1
C 45	15.2	72.4	9009	1	US-07-864-004B-3
C 46	15.2	72.4	9009	1	US-08-251-937A-3
C 47	15.2	72.4	9009	1	US-08-212-133A-1
C 48	15.2	72.4	9009	1	US-08-174-503A-1
C 49	15.2	72.4	9009	1	US-08-174-503A-1
C 50	15.2	72.4	9009	1	US-08-670-707A-1

ALIGNMENTS

RESULT 1
US-08-670-707A-36/C
Sequence 36, Alignment US/08670707A
Patent No. 5853204
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
ADDRESS: 5350 Westmanman Circle Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FILE NAME: C:\COMPU\GEN\US\08670707A.DAT
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,707A
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 07-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
FIRM: Greenlee, Winner and Sullivan, P.C.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE: FIG

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QY      3 TTTATCCAAATTGACACA 20
DB      3116 TTTATCCAAATTGACACA 3099

RESULT 3
US-09-315-179-36/c
US-09-523-656-29/c
Patent No. 6176463
Patent No. 6176463
GENERAL INFORMATION:
APPLICANT: Lollar, John S
TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95H
CURRENT APPLICATION NUMBER: US/09/315,179
EARLIER APPLICATION NUMBER: US/09/315,179
EARLIER APPLICATION NUMBER: U.S. 09/037,601
EARLIER FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: U.S. 08/670,707
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: PCT/US97/11155
EARLIER FILING DATE: 1997-06-26
EARLIER APPLICATION NUMBER: PCT/US94/13200
EARLIER FILING DATE: 1994-03-11
EARLIER APPLICATION NUMBER: U.S. 08/212,133
EARLIER FILING DATE: 1994-03-11
EARLIER APPLICATION NUMBER: U.S. 07/864,004
EARLIER FILING DATE: 1992-04-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
SEQ ID NO 37
SEQ ID NO 402
TYPE: DNA
ORGANISM: Sus scrofa
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (6399)
US-09-315-179-36

Query Match
78.1%, Score 16.4, DB 4, Length 6402;
Best Local Similarity 94.4%, Pred No. 40;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TTTATCCAAATTGACACA 20
DB      3116 TTTATCCAAATTGACACA 3099

RESULT 4
US-09-523-656-29/c
US-09-523-656-29/c
Sequence 29, Application US/09523656
Patent No. 6458563
GENERAL INFORMATION:
APPLICANT: Lollar S., John
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-95H
CURRENT APPLICATION NUMBER: US/09/523,656
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 09/037,601
EARLIER FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 08/670,707
EARLIER FILING DATE: 1996-06-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 6402
TYPE: DNA
ORGANISM: Porcine
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (6399)
US-09-523-656-29

Query Match
78.1%, Score 16.4, DB 4, Length 6402;

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Best Local Similarity 94.4%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TTTATCAATTTCACACA 20
Db 3116 TTTATCAATTTCACACA 3099
|||||

RESULT 5

US-08-962-281-1/c
; Sequence 1, Application US/08962281
; Patent No. 6403356
; GENERAL INFORMATION:
; APPLICANT: You, Li
; APPLICANT: Usher, John J.
; APPLICANT: Nalce, Brenda J. Jiri
; APPLICANT: No. 40
; TITLE OF INVENTION: MUTANT, PENICILLIN G ACYLASES
; FILE REFERENCE: ON0149A (9197F-86)
; CURRENT APPLICATION NUMBER: US/08/962.281
; CURRENT FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 627
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(627)
US-08-962-281-1

Query Match 75.2%; Score 15.8; DB 4; Length 627;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy - 2 CTTATCAATTTCACACA 20
Db 202 CTTATCAATTTCACAAA 184
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RESULT 6

US-09-198-603C-25
; Sequence 25, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: TULLY, Raymond E. Thomas
; APPLICANT: MOVER, Stephen S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; TITLE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198.603C
; CURRENT FILING DATE: 1998-11-24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1211
; TYPE: DNA
; ORGANISM: Mouse
US-09-198-603C-25

Query Match 75.2%; Score 15.8; DB 4; Length 1211;
Best Local Similarity 89.5%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTATCAATTTCACACG 21
Db 56 TTTATCAATTTCACAG 74
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RESULT 7

US-09-198-603C-25

US-09-147-522-5
; Sequence 5, Application US/09147522
; Patent No. 6307069
; GENERAL INFORMATION:
; APPLICANT: MAGAGNIN, SIMONA
; APPLICANT: BENATTI, LUCA
; APPLICANT: CINI, MASSIMO
; APPLICANT: SPECIALE, CARMELA
; APPLICANT: CINI, MASSIMO
; TITLE OF INVENTION: RECOMBINANT KYURENINE-3-HYDROXYLASE ENZYME AND
; TITLE OF INVENTION: PROCESS FOR ITS PREPARATION
; FILE REFERENCE: 0769-0408-OPCT
; CURRENT APPLICATION NUMBER: US/09/147.522
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: PCT/EP7/03589
; EARLIER FILING DATE: 1997-07-03
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)..(1507)
US-09-147-522-5

Query Match 75.2%; Score 15.8; DB 3; Length 5000;
Best Local Similarity 89.5%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTTATCAATTTCACAC 19
Db 2587 ACTTATCAATTTCACAGC 2605
|||||

RESULT 8

US-08-203-532F-1/c
; Sequence 1, Application US/08203532F
; Patent No. 5856121
; GENERAL INFORMATION:
; APPLICANT: Gorecki, David H.
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Growth Arrest Homeobox Gene
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Caltee, Halter, and Griswold
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; RELEASE DATE: 1998-11-24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203.532F
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goltick, Mary E.
; REGISTRATION NUMBER: 34829
; ADDRESS: 10000 Rockledge Drive, #2211/00114
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; TELEX: 980499
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2244 base pairs
; TYPE: nucleic acid

STRAINEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
NAME/KEY: CDS
LOCATION: 197..1108
US-08-203-532F-1

Query Match 73.3%; Score 15.4; DB 2; Length 2244;
Best Local Similarity 94.1%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

OY 1 ACTTATCCAATTTCAC 17
DB 1314 ACTTCTCCAATTTCAC 1298

RESULT 9
US-09-078-465-1/c Location US/09078465
Patent No. 6280949
GENERAL INFORMATION:
APPLICANT: Gorski, David H.
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: Growth Arrest Homeobox Gene
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Calfee, Halter, and Griewold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2668
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-MAY-1998
CLASSIFICATION:
APPLICATION NUMBER: US/09/078,465
PCT-US95-01882A-1
FILING DATE: 24-FEB-1994
APPLICATION NUMBER: US/08/203,532
ATTORNEY/AGENT INFORMATION:
NAME: Goltick, Mary E.
REGISTRATION NUMBER: 34829
REFERENCE/DOCKET NUMBER: 22311/00114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 2244 base pairs
TYPE: nucleic acid
STRAINEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 197..1108
PCT-US95-01882A-1

Query Match 73.3%; Score 15.4; DB 4; Length 2244;
Best Local Similarity 94.1%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

OY 1 ACTTATCCAATTTCAC 17
DB 1314 ACTTCTCCAATTTCAC 1298

RESULT 11
US-08-845-258-3
Sequence 3, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Gorski, David H.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:

STRAINEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
NAME/KEY: CDS
LOCATION: 197..1108
PCT-US95-01882A-1

Query Match 73.3%; Score 15.4; DB 5; Length 2244;
Best Local Similarity 94.1%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

OY 1 ACTTATCCAATTTCAC 17
DB 1314 ACTTCTCCAATTTCAC 1298

RESULT 10
PCT-US95-01882A-1/c
Sequence 1, Application PC/TUS9501882A
GENERAL INFORMATION:
APPLICANT: Gorski, David H.
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: Growth Arrest Homeobox Gene
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Calfee, Halter, and Griewold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2668
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-MAY-1998
CLASSIFICATION:
APPLICATION NUMBER: PCT/US95/01882A
PCT-US95-01882A-1
FILING DATE: 24-FEB-1994
APPLICATION NUMBER: 197..1108
ATTORNEY/AGENT INFORMATION:
NAME: Goltick, Mary E.
REGISTRATION NUMBER: 34829
REFERENCE/DOCKET NUMBER: 22311/00114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 2244 base pairs
TYPE: nucleic acid
STRAINEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 197..1108
PCT-US95-01882A-1

Query Match 73.3%; Score 15.4; DB 5; Length 2244;
Best Local Similarity 94.1%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

OY 1 ACTTATCCAATTTCAC 17
DB 1314 ACTTCTCCAATTTCAC 1298

RESULT 11
US-08-845-258-3
Sequence 3, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Gorski, David H.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-845-258-3

Query Match 73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTATCCAATTTTACACA 20
Db 1819 TTATCCAATTTTACACA 1835

RESULT 12
US-08-845-258-40/C
Sequence 40, Application US/06845258
Patent No. 618376
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
AND TREATMENT OF B. MICROIDI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-845-258-40

Query Match 73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTATCCAATTTTACACA 20
Db 612 TTATCCAATTTTACACA 596

RESULT 13
US-08-990-571-3
Sequence 3, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-990-571-3

Query Match 73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTATCCAATTTTACACA 20
Db 1819 TTATCCAATTTTACACA 1835

RESULT 14
US-08-990-571-40/C
Sequence 40, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

Query Match 73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTATCCAATTTTACACA 20
Db 1819 TTATCCAATTTTACACA 1835

RESULT 14
US-08-990-571-40/C
Sequence 40, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M

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; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; LENGTH: 2430 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-990-571-40

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Query Match          73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred. No. 1.le-02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy  4  TTATCCAATTTTACACA 20
    |||||
Db   612 TTATCCAATTTTACACA 596

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RESULT 15
US-08-723-142A-3
; Sequence 3, Application US/08723142A
; Patent No. 6,866,600
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; AND TREATMENT OF B. MICROIDI INFECTION
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /08/723.142A
; REFERENCE/DOCKET NUMBER: US/08/723.142A
; FILING DATE: 01-DEC-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-723-142A-3

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Query Match          73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred. No. 1.le-02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy  4  TTATCCAATTTTACACA 20
    |||||
Db   1819 TTATCCAATTTTACACA 1835

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Search completed: June 9, 2003, 11:07:40
Job time : 35.5 secs

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GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: June 9, 2003, 09:12:21 | Search time 59.5 seconds

Title: Without alignments

Perfect score: 21

Sequence: 1

Scoring table: IDENTITY_NUC

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgm2_6/pdata/1/pubpna/ECTUS_PUB.seq*
- 3: /cgm2_6/pdata/1/pubpna/US06_PUBCOMB.seq*
- 4: /cgm2_6/pdata/1/pubpna/US07_PUBCOMB.seq*
- 5: /cgm2_6/pdata/1/pubpna/US07_NEW_PUB.seq*
- 6: /cgm2_6/pdata/1/pubpna/ECTUS_PUBCOMB.seq*
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- 14: /cgm2_6/pdata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	21	100.0	712	9	US-10-009-155B-5
5	21	100.0	113604	9	US-10-227-195A-1
6	21	100.0	113604	9	US-10-227-195A-2
7	16.4	78.1	339	10	US-09-867-701-9715
c 8	16.4	78.1	461	9	US-09-918-995-31400
9	16.4	78.1	752	9	US-09-776-724A-22
c 10	16.4	78.1	893	9	US-10-198-846-5479
11	16.4	78.1	180021	10	US-09-846-5534
12	16.4	78.1	368004	9	US-09-846-5534
13	16.4	78.1	180121	9	US-10-329-960-1
14	16.2	77.1	431	9	US-09-818-995-7825
15	16.2	77.1	870	10	US-09-969-708-530
16	16.2	77.1	1273	9	US-10-091-438-105
17	16.2	77.1	1273	10	US-09-764-853-409
18	16.2	77.1	1273	10	US-09-764-877-1010
19	16.2	77.1	1825	9	US-10-198-846-13864

20	16.2	77.1	4656	10	US-09-880-107-2266
c 21	15.8	75.2	615	9	US-09-846-534
22	15.8	75.2	1488	9	US-09-938-842-5708
c 23	15.8	75.2	1763	9	US-09-755-017-3
24	15.8	75.2	4160	9	US-10-050-704-76
c 25	15.8	75.2	5271	12	US-09-822-846-171
26	15.8	75.2	143306	10	US-10-044-090-354
c 27	15.8	75.2	407	9	US-09-729-920-3
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c 29	15.4	73.3	488	9	US-10-198-846-5534
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c 31	15.4	73.3	495	9	US-10-198-846-209
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42	15.4	73.3	912	9	US-10-198-846-2887
c 43	15.4	73.3	912	9	US-10-198-846-2887
44	15.4	73.3	912	9	US-10-198-846-5534
c 45	15.4	73.3	931	9	US-10-198-846-7336

ALIGNMENTS

RESULT 1
US-09-864-761-33139
US-09-864-761-33139 Application US/09864761
PATENT NO. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David R.
APPLICANT: Chem, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Accmcla-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00658
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

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, PRIOR APPLICATION NUMBER: PCT/US01/00670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
, SEQ ID NO 33139
, LENGTH: 372
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AP00120.1
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
, OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.67
, OTHER INFORMATION: EST HUMAN HIT: A165452.1, EVALU0.006+00
, OTHER INFORMATION: SWISSPROT HIT: Q9Y606, EVALU0.006-67
, OTHER INFORMATION: NCBI HIT: G111326220, EVALU0.006+00
US-09-864-761-3463

Query Match 100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 7 ACTTATCCAAATTCACAG 27

RESULT 2
US-09-864-761-3463
, Sequence 3463, Application US/09864761
, Patent No. US20020048763A1
, GENERAL INFORMATION:
, APPLICANT: Penn, Sharon G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wensheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
, CURRENT FILING DATE: 2001-05-23
, CURRENT APPLICATION NUMBER: US 09/864,761
, PRIOR FILING DATE: 2000-02-04
, PRIOR APPLICATION NUMBER: US 60/180,312
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-08-03
, PRIOR APPLICATION NUMBER: US 09/632,366
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/00666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00667
, PRIOR APPLICATION NUMBER: PCT/US01/00664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00668
, PRIOR APPLICATION NUMBER: PCT/US01/00663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00661

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, PRIOR APPLICATION NUMBER: PCT/US01/00670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
, SEQ ID NO 3463
, LENGTH: 450
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AP00052.1
, OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
, OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
, OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
, OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.4
, OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
, OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
, OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
, OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
, OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.89
US-09-864-761-3463

Query Match 100.0%; Score 21; DB 10; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 162 ACTTATCCAAATTCACAG 182

RESULT 3
US-09-864-761-16671
, Sequence 16671, Application US/09864761
, Patent No. US20020048763A1
, GENERAL INFORMATION:
, APPLICANT: Penn, Sharon G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wensheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
, CURRENT FILING DATE: 2001-05-23
, CURRENT APPLICATION NUMBER: US 09/864,761
, PRIOR FILING DATE: 2000-02-04
, PRIOR APPLICATION NUMBER: US 60/180,312
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-08-03
, PRIOR APPLICATION NUMBER: US 09/632,366
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/00666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00667
, PRIOR APPLICATION NUMBER: PCT/US01/00664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00668

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; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 43117
; SEQ ID NO 16671
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000120.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.67
US-09-550-163-1-copy_80_100.rnpb

Query Match 100.0%; Score 21; DB 10; Length 471;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 245 ACTTATCCAAATTCACAG 265

RESULT 4
US-10-000-151B-5
; Sequence 5, Application US/10000151B
; Publication No. US20030013136A1
; INVENTION:
; APPLICANT: Jeffrey R.
; APPLICANT: George, Alfred L.
; TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
; FILE REFERENCE: Vanderbilt Ref No. US20030013136A1 VU0120; Attorney Docket No. US2003
; CURRENT APPLICATION NUMBER: US/10/000,151B
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fatucin version 3.1
; SEQ ID NO 5
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-000-151B-5

Query Match 100.0%; Score 21; DB 9; Length 732;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 80 ACTTATCCAAATTCACAG 100

RESULT 5
US-10-227-195A-1
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103001

Query Match 100.0%; Score 21; DB 9; Length 113604;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 17482 ACTTATCCAAATTCACAG 17502

RESULT 6
US-10-227-195A-2
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103001
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
US-10-227-195A-2

Query Match 100.0%; Score 21; DB 9; Length 113604;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTCACAG 21
Db 17482 ACTTATCCAAATTCACAG 17502

RESULT 7
US-09-867-701-9715
; Sequence 9715, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Aglate, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9715
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9715

Query Match 78.1%; Score 16.4; DB 10; Length 339;

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Best Local Similarity 94.4%; Pred. No. 3.9e+02; Indels 0; Gaps 0; Mismatches 1; Matches 17; Conservative 0;

Oy 1 ACTTATCCCAATTTCACA 18
Db 160 ACTTTTCCCAATTTCACA 177

RESULT 8

US-09-918-995-31400/c
; Sequence 31400, Application US/09918995
; Publication No. US2003007623A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; FILE REFERENCE: 1999-06-06
; NUMBER OF SEQ ID NOS: 380540
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31400
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; LOCATION: (1)-(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31400

Query Match 78.1%; Score 16.4; DB 9; Length 461;
Best Local Similarity 94.4%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 TTATCCCAATTTCACACAG 21
Db 389 TTATCCCAAGTTTCACACAG 372

RESULT 9

US-09-776-724A-22
; Sequence 22, Application US/09776724A
; Publication No. US20030050455A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: P2011
; CURRENT APPLICATION NUMBER: US/09/776,724A
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/180,909
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/669,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: 09/071,613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,873
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875

; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Matchin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-776-724A-22

Query Match 79.1%; Score 16.4; DB 9; Length 752;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ACTTATCCCAATTTCACA 18
Db 116 ACTTTTCCCAATTTCACA 133

RESULT 10

US-10-198-846-2479/c
; Sequence 2479, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Wang, Jongsan
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2479
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 456, 466, 486, 532, 537, 546, 579, 580, 588, 605, 631, 699,
; LOCATION: 700, 707, 709, 710, 723, 726, 742, 746, 754, 792, 804, 805,
; LOCATION: 808, 811, 813, 814, 817, 820, 835, 838, 844,
; LOCATION: 846, 854, 857, 858, 862, 866, 873, 879, 888, 892


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; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2479
Query Match      78.1%; Score 16.4; DB 9; Length 893;
Best Local Similarity 94.4%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTATCCATTTCACACG 21
      |||||
Db 576 TTATCCATTTCACACG 559

RESULT 11
US-10-187-319-36/C
; Sequence 36, Application US/10187319
; Publication No. US2003006878A1
; GENERAL INFORMATION:
; APPLICANT: Loviatar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT INVENTION:
; APPLICANT: Loviatar, John S.
; APPLICATION NUMBER: US/10187,319
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 09/523,656
; FILING DATE: 2000-03-10
; APPLICATION NUMBER: US 09/037,601
; FILING DATE: 1997-03-10
; APPLICATION NUMBER: NO PCT/US97/11155
; FILING DATE: 1997-06-26
; APPLICATION NUMBER: US 08/670,707
; FILING DATE: 1996-06-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenlee, Lorance L.
; REGISTRATION NUMBER: 27,494
; ADDRESS: 10000 E. 1st Avenue, Suite 595K
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6402 base pairs
; TYPE: nucleic acid
; STRATEGY: full-length
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Pig
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6402
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-10-187-319-36
Query Match      78.1%; Score 16.4; DB 9; Length 6402;
Best Local Similarity 94.4%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TTATTCATTTCACACG 20
      |||||
Db 3116 TTATTCATTTCACACG 3099

RESULT 12
US-09-949-654-3
; Sequence 3, Application US/09949654
; Patent No. US20020127644A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 09-11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 368004
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(368004)
; OTHER INFORMATION: n = A,T,C or G
; OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3

Qy 4 TTATCCATTTCACACG 21
      |||||
Db 175073 TTATCCATTTCACACG 175090

Query Match      78.1%; Score 16.4; DB 10; Length 368004;
Best Local Similarity 94.4%; Pred. No. 1.1e-03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
US-10-328-960-1
; Sequence 1, Application US/10328960
; Publication No. US20030099277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fra
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: SeqScribe, Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1830121
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10150)..(10150)
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? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (80024)..(80024)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (100091)..(100091)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (102696)..(102696)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (105121)..(105121)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (107248)..(107248)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (117136)..(117136)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (119750)..(119750)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (119524)..(119524)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (120038)..(120038)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (121344)..(121344)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (122167)..(122167)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (122336)..(122336)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (131340)..(131340)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (131360)..(131360)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (139910)..(139910)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (140398)..(140398)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (142750)..(142750)
? OTHER INFORMATION: n equals a, t, g or c
? NAME/KEY: misc_feature
? LOCATION: (145058)..(145058)
? OTHER INFORMATION: n equals a, t, g or c
? FEATURE:

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; NAME/KEY: misc feature
 ; LOCATION: (145171)..(145171)
 ; OTHER INFORMATION: n equals a, t, g or c
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (145942)..(145942)
 ; OTHER INFORMATION: n equals a, t, g or c
 ; NAME/KEY: misc feature
 ; LOCATION: (147197)..(147197)
 ; OTHER INFORMATION: n equals a, t, g or c
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (150841)..(150841)
 ; OTHER INFORMATION: n equals a, t, g or c
 ; NAME/KEY: misc feature
 ; LOCATION: (152500)..(152500)
 ; OTHER INFORMATION: n equals a, t, g or c
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (152530)..(152530)

Query Match 78.1%; Score 16.4; DB 9; Length 1830121;
 Best Local Similarity 94.1%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 1; Mismatches 1;
 Qy 1 ACTTTATCCAAATTTTCAC 18
 Db 161151 ACTTTATCCAAATTTTCAC 161168

RESULT 14
 US-09-918-995-7825
 ; Sequence 7825, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM THE GENOMES OF SEVERAL VARIOUS CHINA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 725
 ; LENGTH: 431
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-918-995-7825
 Query Match 77.1%; Score 16.2; DB 9; Length 431;
 Best Local Similarity 85.7%; Pred. No. 4.7e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ACTTTATCCAAATTTTCAC 21
 Db 83 ACCTGATCCAAATTTTCAC 103

RESULT 15
 US-09-969-708-530
 ; Sequence 530, Application US/09969708
 ; Patent No. US20020102532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Augustus, Meena
 ; TITLE OF INVENTION: Cancer
 ; FILE REFERENCE: 469290-70
 ; CURRENT APPLICATION NUMBER: US/09/969,708
 ; CURRENT FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: US/60/237,606
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237,608
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: US/60/237,425
 ; PRIOR FILING DATE: 2000-10-03
 ; NUMBER OF SEQ ID NOS: 658
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 510
 ; LENGTH: 870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-969-708-530

Query Match 77.1%; Score 16.2; DB 10; Length 870;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ACTTTATCCAAATTTTCAC 21
 Db 524 ACTTTATCCAAATTTTCAC 544

Search completed: June 9, 2003, 12:10:08
 Job time : 124.5 secs

Result	No.	Score	Query	Match	Length	ID	Description
C	1	21	100.0	311	10	AM859303	AM859303 MR3-SN006
C	2	21	100.0	746	12	BG221966	BG221966 RST41783
C	3	18.1	100.0	803	12	BZ209163	BZ209163 RST37654
C	5	18.4	87.6	561	17	AO785139	AO785139 X33053-X
C	6	18.4	87.6	565	14	BO506232	BO506232 RST61367

Email: asimpson@ludwig.org, br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scriptu/gethtml2.pl?cl=et2=MR3-SN0067-240
 000-006-f1163=2000-04-24&c=1)
 seq primer: puc 18 forward: 11
 High quality sequence stop: 74
 Location/Qualifiers

FEATURES

source
 1..311
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="SN0067"
 /dev_stage="Adult-onset normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORRESTES PCR (U.S. Letters Patent Application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcribed of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 60 a 80 c 76 g 95 c

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 311;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTATCCCAATTCACAG 21
 |||||||
 Db 176 ACTTATCCCAATTCACAG 156

RESULT 2

BG221966 746 bp mRNA linear EST 21-APR-2001
 LOCUS R5272654 Atherays RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG221966
 VERSION BG221966.1 GI:13747987
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
 ,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
 ,J., Danzig,J., and Ducat,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel: 216 431 9500
 Fax: 216 361 9596
 Email: scaine@athersys.com
 High quality sequence stop: 547.
 Location/Qualifiers

FEATURES

source
 1..746
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Atherys RAGE Library"
 /dev_stage="Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression",
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 241 a 138 c 123 g 243 t 1 others
 ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 746;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTATCCCAATTCACAG 21
 |||||||
 Db 532 ACTTATCCCAATTCACAG 552

RESULT 3

BG208163 803 bp mRNA linear EST 21-APR-2001
 LOCUS R5272654 Atherays RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG208163
 VERSION BG208163.1 GI:13729850
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (base 1 to 803)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mayer,R., Smith
 ,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
 ,J., Danzig,J., and Ducat,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel: 216 431 9500
 Fax: 216 361 9596
 Email: scaine@athersys.com
 High quality sequence stop: 550.
 Location/Qualifiers

FEATURES

source
 1..803
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Atherys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT

ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 803;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACTTATCCCAATTCACAG 21
 |||||||
 Db 682 ACTTATCCCAATTCACAG 682

RESULT 4

B8847728 419 bp mRNA linear EST 26-SEP-2000
 LOCUS u93d05.y1 Soares mouse 3JMS Mus musculus cDNA clone IMAGE:3414729
 DEFINITION 5', mRNA sequence.
 ACCESSION B8847728
 VERSION B8847728.1 GI:10306067
 KEYWORDS EST.
 SOURCE house mouse.

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE          1 (bases 1 to 419)
JOURNAL        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1090541
Seq primer: -40RP from Gibco.
FEATURES      Location/Qualifiers
source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3414729"
/clone_lib="Soares mouse 3BMS"
/sex="male"
/tissue_type="Spleen"
/lab_host="DH10B"
BASE COUNT    136 a 62 c 90 g 131 t
ORIGIN
Query Match      87.6%; Score 18.4; DB 12; Length 419;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTTTTCAATTTCACCA 20
Db 217 ACTTTTCAATTTCACCA 198

RESULT 5
LOCUS      A0785939
DEFINITION HS_3053_A2 G02 T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate=3053 Col=4 Row=M, DNA sequence.
ACCESSION  A0785939
VERSION     A0785939.1
KEYWORDS    GSS.
SOURCE      GSS.
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      1 (bases 1 to 561)
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Le-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahaiars GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3616

FEATURES      Location/Qualifiers
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3053 Col=4 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
72 g 211 t 5 others
BASE COUNT    181 a 92 c
ORIGIN
Query Match      87.6%; Score 18.4; DB 17; Length 561;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTTTATCGAATTCACGAG 21
Db 472 CTTTATCGAATTCACGAG 491

RESULT 6
LOCUS      B0506222
DEFINITION B0506222 Generation of a set of potato cDNA clones for microarray analysis using mixed potato tissues Solanum tuberosum cDNA clone STN0192 5' and 3' UTRs.
ACCESSION  B0506222
VERSION     B0506222.2
KEYWORDS    EST.
SOURCE      potato.
ORGANISM    Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Solanaceae; Solanaceae; Solanaceae; Solanaceae; Solanaceae; Solanaceae;
Asteridae; eusteleids 1; Solanales; Solanales; Solanales; Solanales;
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002) This sequence version replaced gi:21385091.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@igr.org
This clone is available through the Research Genetics; contact the
Research Genetics for further information 1-800-711-6195 or
Research Genetics
Seq primer: T3
FEATURES      Location/Qualifiers
source
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STN0192"
/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes

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BASE COUNT      200 a 159 c 124 g 183 t
ORIGIN
Query Match      87.6%; Score 18.4; DB 14; Length 666;
Best Local Similarity 95.0%; Pred. No. 6.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTCACACA 20
    |||||
Db 229 ACTTTATCCAAATTCACACA 248

RESULT 7
BG595346
LOCUS BG595346
DEFINITION EST494024 cSTS Solanum tuberosum cDNA clone cSTS1019 5' sequence, mRNA sequence.
ACCESSION BG595346
VERSION BG595346.1 GI:13613486
SOURCE EST.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphorbia; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 689)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemiango, A.,
Gouffier, O., and ESTs from sprouting potato eyes
Contact: Cathy Ronning
Unpublished (2000)
The Institute for Genomic Research
For clone info: please contact Rusearch Genetics, Libraries
Division tel 1-800-771-6195, email cdna@reagen.com
Seq primer: M13-R
LOCAL QUALIFIERS
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS1019"
/clone_lib="cSTS"
/tissue_type="sprouting eyes from tubers"
/tissue_age="4 weeks post harvest"
/lab_pos="sq1a"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of uproutng eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

BASE COUNT      209 a 164 c 128 g 188 t
ORIGIN
Query Match      95.6%; Score 18.4; DB 12; Length 689;
Best Local Similarity 97.0%; Pred. No. 6.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTCACACA 20
    |||||
Db 229 ACTTTATCCAAATTCACACA 248

RESULT 8
BF092401/c
LOCUS BF092401
DEFINITION BF092401 109-120900-202-111 TNO109 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF092401
VERSION BF092401.1 GI:10898215
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191)
Dias, Neco, E., Garcia, Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Rago, M.A., Borchi, A., Costa, A., Basso, A., Basso, D.H.,
Cotter, C.H., de Almeida, P., Bucher, P., Jongsom, C.V. O'Hare,
Brunein, A., de Oliveira, P., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2028663 Simpson, A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scipos/gethtml2.pl?l=62-MR4-TNO109-120
900-202-111&t=2000-09-12&t=1)
Seq primer: puc 18 forward
High quality sequence stop: 190.
LOCAL QUALIFIERS
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TNO109"
/dev_stage="Adult"
/notes="organ: testis normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; This library was made by cloning products
from testis tissue. ORGSTATS PCR U.S. vector per
No.136.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT      55 a 47 c 42 g 47 t
ORIGIN
Query Match      94.9%; Score 17.8; DB 12; Length 191;
Best Local Similarity 90.5%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTTTATCCAAATTCACACG 21
    |||||
Db 101 ACTTTATCCAAATTCACACG 81

RESULT 9
BG152818/c
LOCUS BG152818
DEFINITION BG152818 358 bp mRNA linear EST 05-FEB-2001
similar to SP:RSAY.HMAN.P2090 40S RIBOSOMAL PROTEIN S4, Y
ISOFORM 1, mRNA sequence.
ACCESSION BG152818
VERSION BG152818.1 GI:12664848
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 358)
NCI, nci.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

```



```

Query Match      84.8%; Score 17.8; DB 13; Length 389;
Best Local Similarity 90.5%; Pred. No.1e-03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
    |||||
Db 274 ACTTATCCAAATTTTCACAG 254

RESULT 12
AW784520/c 396 bp mRNA linear EST 22-MAY-2000
LOCUS ZB64406.5, mRNA sequence.
ACCESSION AW784520.1 GI:7838968
VERSION AW784520.1
KEYWORDS
ORGANISM Canis familiaris
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 396)
AUTHORS McCombie M.R., See, L.H., Baker, J.P., Bahret, A., Dedhia, M.N., de la
Bastide, M., Huang, E.N., King, L., Kirchoff, K.A., Miller, B.,
Nacimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, M.A.,
Shah, R.S., Shklier, M., Spiegel, L.A., Toth, K., Vill, M.D. and Hannan
G.J.
Expressed sequence tags from Canis familiaris (dog)
UNCLUSTED 120001
UPDATE 120001
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: wmc@mcgill.org
URL: http://www.mcgill.org
Seq primer: -40M13RevUniv
High quality sequence stop: 396.
FEATURES
Location/Qualifiers
1..396
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone_lib="Canis cDNAu from mdck cells"
/notes="Vector: Lambda Zap II; The library was provided by
Greg Hannan (Cold Spring Harbor Laboratory). This
library is oligo(dT) primed using stratagene zap cDNA
synthesis kit. It was made from exponentially growing mdck
cells. Please contact Greg Hannan (hannan@cshl.org) with
any library related inquiries."
BASE COUNT 71 a 125 c 82 g 116 t
ORIGIN
Query Match      84.8%; Score 17.8; DB 10; Length 396;
Best Local Similarity 90.5%; Pred. No.1e-03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
    |||||
Db 100 ACTTATCCAAATTTTCACAG 80

RESULT 13
BF091642/c 427 bp mRNA linear EST 19-OCT-2000
LOCUS W600045-130900-012-a09-TN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF091642.1 GI:10897352
VERSION BF091642.1
KEYWORDS EST.
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Dias Neto E.B., Garcia Correa R., Verjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.N.F., Zago, M.A., Bordin, S., Costa, F.F., D.H.,
Goldstein, H., Goto, T., Kikuchi, A., Kishimoto, A., Kishimoto, C.,
Bruneau, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2002663 Simpson A.J.G.
LABORATORY Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
URL: http://www.ludwig.org.br
Project: This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?c1=6t2-MR1-TN0045-130
900-012-a09&t3=2000-09-13&t4=1
900-012-a09&t3=2000-09-13&t4=1
Seq primer: puc 18 forward
High quality sequence stop: 427.
FEATURES
Location/Qualifiers
1..427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TN0045"
/dev_stage="Adult"
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No. 96/7110 to the Ludwig Institute for Cancer Research)
No. 96/7110 to the Ludwig Institute for Cancer Research)
No. 96/7110 to the Ludwig Institute for Cancer Research)
tissue mRNA and cDNA amplification were performed under
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Db 338 ACTTATCCAAATTTTCACAG 318

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LOCUS CIT-HSP-2337A2.TF CIT-HSP Homo sapiens genomic clone 2337A2, DNA
DEFINITION
ACCESSION AQ037472
VERSION AQ037472.1 GI:3303304
KEYWORDS GSS, EST, human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Adams, M.D., Rounley, S.D., Zhao, S., Field, C.E., Baes, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Kane, J., and Venter, A.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CIT-HSP-2337A2.TR
Contact: Mark Adams
Department of Eukaryotic Genomics

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 427)
AUTHORS Dias Neto E.B., Garcia Correa R., Verjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.N.F., Zago, M.A., Bordin, S., Costa, F.F., D.H.,
Goldstein, H., Goto, T., Kikuchi, A., Kishimoto, A., Kishimoto, C.,
Bruneau, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2002663 Simpson A.J.G.
LABORATORY Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
URL: http://www.ludwig.org.br
Project: This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?c1=6t2-MR1-TN0045-130
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Site 2: SmaI; A mini-library was made by cloning products
derived from ORFESTES PCR (U.S. letters Patent application
No. 96/7110 to the Ludwig Institute for Cancer Research)
No. 96/7110 to the Ludwig Institute for Cancer Research)
No. 96/7110 to the Ludwig Institute for Cancer Research)
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 116 a 105 c 93 g 113 t
ORIGIN
Query Match      84.8%; Score 17.8; DB 12; Length 427;
Best Local Similarity 90.5%; Pred. No.1e-03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACTTATCCAAATTTTCACAG 21
    |||||
Db 338 ACTTATCCAAATTTTCACAG 318

RESULT 14
AQ037472 429 bp DNA linear GSS 11-JUL-1998
LOCUS CIT-HSP-2337A2.TF CIT-HSP Homo sapiens genomic clone 2337A2, DNA
DEFINITION
ACCESSION AQ037472
VERSION AQ037472.1 GI:3303304
KEYWORDS GSS, EST, human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Adams, M.D., Rounley, S.D., Zhao, S., Field, C.E., Baes, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Kane, J., and Venter, A.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CIT-HSP-2337A2.TR
Contact: Mark Adams
Department of Eukaryotic Genomics

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Job time : 889 secs

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GenCore version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 11:54:30 ; Search time 1051 Seconds

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	84	46.4	746	12	BG221966 RST41783

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728	16	8.8	778	17	BH477252	BH477252	C 801	16	8.8	883	12	BF672604	BF672604	602152186
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ALIGNMENTS

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CHANNEL PROTEIN 1, mRNA sequence.
A1654552.1 GI:575363
EST.
Human
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 410)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
AUTHORS Robert Strausberg, Ph.D.
TITLE NCI-CGAP Project
COMMENT Email: cgapb@nci.nih.gov
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

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Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://www.genome.gov/90000000/ncicgaphom.html
Insert Length: 770 Std Error: 0.00
Seq primer: -40UP from Gibco.
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/label="type="pooled germ cell tumors"
/label="host="DH10B"
/notes="Vector: p7730-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
88 circles were made in vitro. Following HAP purification,
this DNA was added to the library. The library was then
amplified by PCR using the following primers:
1257096-1259631, 1469064-1470983, and 1475592-1476743.
1257096-1259631, 1469064-1470983, and 1475592-1476743.
Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 120 a 93 c 93 g 104 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1,78-71;
Matches 151; Conservative 0; Mismatches 0; Gaps 0;
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Db 18 GAGCTCTCCGAGAGATTTTATTCTATATGACCAATTCGGCCGAGACACACAGCT 77
Qy 91 GAGCAGAGCGCTCCGACGCAAGTGTGATGTCGAGACTTCTACTATCTCTCTGAC 150
Db 78 GAGCAGAGCGCTCCGACGCAAGTGTGATGTCGAGACTTCTACTATCTCTCTGAC 137
Qy 151 CTCATGTCGATGTTGAATGTCCTTTCA 181
Db 138 CTCATGTCGATGTTGAATGTCCTTTCA 168
RESULT 2
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CHANNEL PROTEIN 1, mRNA sequence.
A1654552.1 GI:4739531
EST.
Human
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 429)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
AUTHORS Robert Strausberg, Ph.D.
TITLE NCI-CGAP Project
COMMENT Email: cgapb@nci.nih.gov
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

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www.bio.llnl.gov/hbm/image/image.html
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 High quality sequence stop: 411.

FEATURES

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Location/Qualifiers
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 127 a 100 c 97 g 104 t 1 others

Query Match 81.4%; Score 151; DB 9; Length 429;
 Best Local Similarity 100.0%; Pred No. 17a-71;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GAGCTCTCCGAGAGATTTTATTCTATATGGCAATTCGGCCGAGACACACAGCT 90
 Db 12 GAGCTCTCCGAGAGATTTTATTCTATATGGCAATTCGGCCGAGACACACAGCT 71
 QY 91 GAGCAGAGCCCTCCGAGCAAGATTCGTCGAGACTTCTACTATCTCTCTCTAC 150
 Db 72 GAGCAGAGCCCTCCGAGCAAGATTCGTCGAGACTTCTACTATCTCTCTCTAC 131
 QY 151 CTCATGTCGATGATGGAATGTCCTCTTTCA 181
 Db 132 CTCATGTCGATGATGGAATGTCCTCTTTCA 162

RESULT 3
 A1246239
 LOCUS q129g04.x1 Soares NHRMPU_S1 Homo sapiens cDNA clone IMAGE:1857942
 DEFINITION 3' similar to SW:MINK HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN 1; mRNA sequence.

ACCESSION A1246239.1 GI:3841636
 VERSION EST
 KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI (bases 1 to 372)
 TITLE NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgsaps-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 400P from Gibco
 Std Error: 0.00
 High quality sequence stop: 365.

Location/Qualifiers

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FEATURES

source

Location/Qualifiers

Pregnant uterus"

/lab_host="DH108"
 /note="Mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBHH19M) were mixed, and 5000 clones made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization. The pools of 5000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 115 a 89 c 86 g 82 t

ORIGIN

Query Match 79.0%; Score 143; DB 9; Length 372;
 Best Local Similarity 100.0%; Pred No. 34a-67;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CCGAAGGATTTTATTCTATATGGCAATTCGGCCGAGACACACACAGCTGAGCAAG 98
 Db 1 CCGAAGGATTTTATTCTATATGGCAATTCGGCCGAGACACACACAGCTGAGCAAG 60
 QY 99 GCGCTTCAGCAAGATTCGTCGAGACTTCTACTATGTCATGTCCTGCTCCTGCT 158
 Db 61 GCGCTTCAGCAAGATTCGTCGAGACTTCTACTATGTCATGTCCTGCTCCTGCT 120
 QY 159 GATGATTGGAATGTTCTTTCTTA 181
 Db 121 GATGATTGGAATGTTCTTTCTTA 143

RESULT 4

LOCUS

A1339609
 q42a07.x1 Soares NHRMPU_S1 Homo sapiens cDNA clone IMAGE:1935156
 DEFINITION 3' similar to SW:MINK HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN 1; mRNA sequence.

ACCESSION A1339609
 VERSION EST
 KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI (bases 1 to 391)
 TITLE NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgsaps-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -400P from Gibco
 High quality sequence stop: 380.

FEATURES

source

Location/Qualifiers
 1..391
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

/clone_lib="Soares NHRMPU_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and

Pregnant uterus"

/note="Organ: mixed (see below); Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBHH19M) were mixed, and 5000 clones made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

```

BASE COUNT      119 a   93 c   93 g   86 t
ORIGIN
Query Match
Best Local Similarity 65.7%; Score 119; DB 9; Length 391;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GACAAATTCGCCAGACACACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 122
DB 34 GACAAATTCGCCAGACACACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 93

QY 123 TGAGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
DB 94 TGAGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152

RESULT 5
LOCUS      RG208163/c      803 bp      mRNA      linear      EST 21-APR-2001
DEFINITION R57127654 Atherysys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  RG208163
VERSION     RG208163.1 GI:13729850
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 803)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
TITLE     Creation of genome-wide protein expression libraries using random
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
            Atherysys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scai@atherysys.com
            High quality sequence stop: 550.
            Location/Qualifiers
                1..803
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_library="Atherysys RAGE Library"
                /cell_line="HT1080"
                /note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."
BASE COUNT      222 a   172 c   171 g   238 t
ORIGIN
Query Match
Best Local Similarity 64.6%; Score 117; DB 12; Length 803;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ACATATTCGCCAGACACACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 124
DB 617 ACATATTCGCCAGACACACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 558

QY 125 AGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
DB 94 TGAGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152

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557 AGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
DB 94 TGAGAACTTCCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152

RESULT 6
LOCUS      RG221966      746 bp      mRNA      linear      EST 21-APR-2001
DEFINITION R5714783 Atherysys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  RG221966
VERSION     RG221966.1 GI:13747987
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 746)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
TITLE     Creation of genome-wide protein expression libraries using random
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
            Atherysys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scai@atherysys.com
            High quality sequence stop: 547.
            Location/Qualifiers
                1..746
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_library="Atherysys RAGE Library"
                /cell_line="HT1080"
                /note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."
BASE COUNT      241 a   138 c   123 g   243 t   1 others
ORIGIN
Query Match
Best Local Similarity 46.4%; Score 84; DB 12; Length 746;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTTATCCATTTCACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 60
DB 532 ACTTATCCATTTCACACAGCTGACGAGAGGCGCTTCGACGCAAGTGTATGC 591

QY 61 ATGACCAATTCGGCGCCAGACAC 84
DB 592 ATGACCAATTCGGCGCCAGACAC 615

RESULT 7
LOCUS      AM869303/c      311 bp      mRNA      linear      EST 22-MAY-2000
DEFINITION MR3-SN0067-240400-006-f11 SN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM869303
VERSION     AM869303.1 GI:8003356
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 311)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

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[illegible]

[illegible]

Insert Length: 968 Std Error: 0.00
Seq. Pattern: - - - - -
High quality sequence stop: 281.

FEATURES

Location/Qualifiers

1..365

/organism="Homo sapiens"

/db_xref="GDB:3787914"

/db_xref="taxon:9606"

/clone="MAGE:234793"

/sex="male" Soares fetal liver spleen INFILS"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: Liver and Spleen; Vector: p7773D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dn) primer

and the 2nd strand was synthesized with a modified Eco RI

double-stranded cDNA was ligated into Eco RI-digested

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified p7773 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

71 c 71 g 109 t

BASE COUNT 105 a

ORIGIN

Query Match 11.6%; Score 21; DB 14; Length 365;

Best Local Similarity 100.0%; Pred. No. 1; 3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 GAGAACTCTACTATGTCATC 144

Db 322 GAGAACTCTACTATGTCATC 342

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Qy 27

Db 209

GGAGAGCGTCTCCGAGG 45

GGAGAGCGTCTCCGAGG 191

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RESULT 17

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

Db

GGAGAGCGTCTCCGAGG 45

GGAGAGCGTCTCCGAGG 262

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RESULT 18

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

Db

GGAGAGCGTCTCCGAGG 45

GGAGAGCGTCTCCGAGG 262

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RESULT 19

LOCUS

DEFINITION

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.html>) For BAC library
availability, please contact Pinter de Jong (pdj@chongmail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/orderinginformation.html>). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 44 row: E column: 10
Seq primer: 77
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..539
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCw"
/db_xref="taxon:10116"
/clones="CH230-44E10"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCw) BAC library produced by
Pinter de Jong"

BASE COUNT 175 a 70 c 91 g 199 t

ORIGIN

Query Match 10.5%; Score 19; DB 17; Length 539;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GAAGGATTTTATTACTTA 59

Db 193 GAAGGATTTTATTACTTA 211

RESULT 19

BH302149

DEFINITION CH230-85A14.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-85A14, DNA sequence.

ACCESSION BH302149

VERSION BH302149.1 GI:17214557

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1. (bases 1 to 799) Shatman,S., Tsegaye,G., Geer,K., Shvartsbeyn
Zhao,S., Shetty,J., Gervett,M., Russell,D., Chen,D., Riggs,P., de
Jong,P. and Fraser,C.W.

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL Unpublished (1999)

COMMENT Other GS8s: CH230-85A14.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9122 Corporate Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.html>). For BAC library

availability, please contact Pinter de Jong (pdj@chongmail.cho.org).

(<http://www.chori.org/bacpac/orderinginformation.html>). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 85 row: A column: 14

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..799
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCw"
/db_xref="taxon:10116"
/clones="CH230-44E10"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCw) BAC library produced by
Pinter de Jong"

BASE COUNT 247 a 115 c 131 g 306 t

ORIGIN

Query Match 10.5%; Score 19; DB 17; Length 799;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GAAGGATTTTATTACTTA 59

Db 180 GAAGGATTTTATTACTTA 198

RESULT 20

AL557074

DEFINITION AL557074 LTI_FU012_TCI Homo sapiens cDNA clone CS00H0051023 5 prime
sequence.

ACCESSION AL557074.1 GI:12900327

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. (bases 1 to 938) Li,H.B., Grubb,J., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: sequencage@genoscope.cns.fr; Web : www.genoscope.cns.fr.

FEATURES

source

Location/Qualifiers
1..938
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS00H005Y023"
/clone_lib="LTI_FU012_TCI"
/tissue_type="T cell from T cell leukemia"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-stranded cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
Library was constructed by Life Technologies. Contact :
Feng Liang Life Technologies, a division of Invitrogen
9800 Medical Center Drive Rockville, Maryland 20850 USA
Fax: 301 591 7200 Email: liang@lifetech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 169 a 295 c 319 g 153 t 2 others

ORIGIN

Query Match 10.5%; Score 19; DB 9; Length 938;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 GAGGCCCTCCAGCCCAAG 115

Db 816 GAGGCCCTCCAGCCCAAG 834


```

/dev stage="34 years old"
/lab="SOLR (in resistant)"
/note="Vector: Bluescript SK+; Site 1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old.
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Cuscom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
et al. from the Schizophrenia Genetics Research Institute of
NIH. From the Brained Individual with Psychotic
Diseases (Unpublished) Stanley Neurology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."

BASE COUNT      143 a   66 c
ORIGIN
Query Match      9.9%; Score 18; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 ATTTTATTACTTATG 63
Db 70 ATTTTATTACTTATG 87

RESULT 26
LOCUS      B478577      419 bp      mRNA      linear      EST 28-AUG-2000
DEFINITION      162895 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION      B478577.1 GI:9598110
VERSION
KEYWORDS
SOURCE
ORGANISM      Bos taurus
REFERENCE
AUTHORS      Sonategard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
TITLE      Expressed Sequence Tags from a normalized bovine mammary
cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Sonategard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tad@arl1.barc.usda.gov
Small scale cDNA library created and called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCGACGTCAGCAG
Plate: 21 row: N column: 7
Seq primer: ATTACGAGCTATGAG.

FEATURES
source
1..419
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="vector; pcwv; spornv; Site 1: NotI; Site 2: SalI;
Library: Schizophrenia Genetics Research Institute of NIH;
Tissues at eight physiological, developmental, and disease
states."

BASE COUNT      118 a   77 c   112 g   112 t
ORIGIN
Query Match      9.9%; Score 18; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GATTTTATTACTTAT 62
Db 318 GATTTTATTACTTAT 301

RESULT 28
LOCUS      BE941069      471 bp      mRNA      linear      EST 03-OCT-2000
DEFINITION      BE941069 MHMG Medicago truncatula cDNA clone pMGHG-2824, mRNA
sequence.
ACCESSION      BE941069
VERSION      BE941069.1 GI:10518828
KEYWORDS
SOURCE      Medicago truncatula
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 471)

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/lab_host="E. coli XL Gold"
/seq_vector="pBluescriptII SK(+)"
/seq_lib="Genomic DNA library from Wang/Bonhert lab"
BASE COUNT      115 a 164 c 171 g 130 t
ORIGIN
Query Match      9.9%; Score 18; DB 9; Length 580;
Best Local Similarity 100.0%; Pred. No. 62; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CCGTGAAGACGCTCTCC 40
|||||
DB 427 CCGTGAAGACGCTCTCC 444

RESULT 31
AG009962/c
LOCUS      Homo sapiens genomic DNA, 582 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
sequence.
ACCESSION AG009962 AG003773
VERSION AG009962.1 GI:3289948
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T485XN.
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REVISION (bases 1 to 682)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@jst.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754675.
AG003773; Submitted (07-Jan-1998).
FEATURES
source
1..682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q"
/clone="T485XN"
BASE COUNT      153 a 102 c 218 g 207 t 2 others
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 682;
Best Local Similarity 100.0%; Pred. No. 63; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GAACACACAGCTGAGCA 95
|||||
DB 219 GAACACACAGCTGAGCA 202

RESULT 32
AG009955
LOCUS      Homo sapiens genomic DNA, 690 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
sequence.
ACCESSION AG009955 AG003765
VERSION AG009955.1 GI:3289941
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T485XN.
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REVISION (bases 1 to 692)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@jst.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754671.
AG003765; Submitted (07-Jan-1998).
FEATURES
source
1..692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q"
/clone="T485XN"
BASE COUNT      187 a 184 c 136 g 182 t 3 others
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 692;
Best Local Similarity 100.0%; Pred. No. 63; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GAACACACAGCTGAGCA 95
|||||
DB 664 GAACACACAGCTGAGCA 681

```

```

TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REVISION (bases 1 to 692)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@jst.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754668.
AG003765; Submitted (07-Jan-1998).
FEATURES
source
1..690
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q"
/clone="T485XN"
BASE COUNT      261 a 133 c 129 g 140 t 7 others
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 690;
Best Local Similarity 100.0%; Pred. No. 63; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GAACACACAGCTGAGCA 95
|||||
DB 81 GAACACACAGCTGAGCA 98

RESULT 33
AG009958
LOCUS      Homo sapiens genomic DNA, 692 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
sequence.
ACCESSION AG009958 AG003769
VERSION AG009958.1 GI:3289944
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T485XN.
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REVISION (bases 1 to 692)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@jst.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754671.
AG003769; Submitted (07-Jan-1998).
FEATURES
source
1..692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q"
/clone="T485XN"
BASE COUNT      187 a 184 c 136 g 182 t 3 others
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 692;
Best Local Similarity 100.0%; Pred. No. 63; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 GAACACACAGCTGAGCA 95
|||||
DB 664 GAACACACAGCTGAGCA 681

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```

RESULT 34
AG009557
LOCUS Homo sapiens genomic DNA, 21q region, clone: T485XN, linear, GSS 14-APR-1999
DEFINITION sequence.
ACCESSION AG009557
VERSION AG009557.1 GI:3289943
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T485XN.
ORGANISM Homo sapiens
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS 1 (bases 1 to 700)
JOURNAL Mammalia, Eutheria: Primates, Catarrhini, Hominoidea, Homo.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS 2 (bases 1 to 700)
JOURNAL Mammalia, Eutheria: Primates, Catarrhini, Hominoidea, Homo.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754670.
AG003770: Submitted (07-Jan-1998).
FEATURES
    source
        Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="21"
            /map="21q"
            /clones="T485XN"
BASE COUNT 193 a 203 c 127 g 171 t 6 others
ORIGIN
    Query Match 9.9%, Score 18; DB 17; Length 700;
    Best Local Similarity 100.0%; Pred. No. 63;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 GACACACACGCTGACCA 95
Db 572 GACACACACGCTGACCA 589

RESULT 35
AG009559
LOCUS Homo sapiens genomic DNA, 702 bp, DNA, linear, GSS 14-APR-1999
DEFINITION sequence.
ACCESSION AG003770
VERSION AG009559.1 GI:3289945
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T485XN.
ORGANISM Homo sapiens
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS 1 (bases 1 to 702)
JOURNAL Mammalia, Eutheria: Primates, Catarrhini, Hominoidea, Homo.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS 2 (bases 1 to 702)
JOURNAL Mammalia, Eutheria: Primates, Catarrhini, Hominoidea, Homo.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2754672.
AG003770: Submitted (07-Jan-1998).
FEATURES
    source
        Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="21"
            /map="21q"
            /clones="T485XN"
BASE COUNT 193 a 203 c 127 g 171 t 6 others
ORIGIN
    Query Match 9.9%, Score 18; DB 17; Length 700;
    Best Local Similarity 100.0%; Pred. No. 63;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 GACACACACGCTGACCA 95
Db 572 GACACACACGCTGACCA 589

RESULT 36
AG009560
LOCUS Homo sapiens genomic DNA, 704 bp, DNA, linear, GSS 14-DEC-2001
DEFINITION sequence.
ACCESSION BH556024
VERSION BH556024.1 GI:17807804
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
AUTHORS Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
TITLE Other GSSs: BGGW27TR
JOURNAL Contact: Chris Town
COMMENT 9712 Medical Center Drive, Rockville, MD 20850, USA.
    Tel: 301-838-3523
    Fax: 301-838-0208
    Email: cdtown@igrr.org
    DNA is from a doubled haploid provided by Tom Osborn.
    Seq primer: TP
    Class: single ends
    Location/Qualifiers
        1..704
        /organism="Brassica oleracea"
        /strain="TO1000DH3"
        /db_xref="taxon:3712"
        /clone="BGGW27"
        /accession="BGGW27"
        /notes="ProS1, Site 1, BarXI, 2-3 kb sheared genomic DNA inserted into pGDS1 using BstXI linkers"
BASE COUNT 131 a 180 c 139 g 254 t
ORIGIN
    Query Match 9.9%, Score 18; DB 17; Length 704;
    Best Local Similarity 100.0%; Pred. No. 64;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 AAAGTGTGATGCTGAGAAC 129
Db 389 AAAGTGTGATGCTGAGAAC 372

RESULT 37
AQ362915
LOCUS Oryza sativa genomic clone, 708 bp, DNA, linear, GSS 16-DEC-1999
DEFINITION nxbs0051A06f, CUGI Rice BAC Library Oryza sativa genomic clone
ACCESSION nxbs0051A06f
VERSION nxbs0051A06f.1
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
REFERENCE
    Query Match 9.9%, Score 18; DB 17; Length 704;
    Best Local Similarity 100.0%; Pred. No. 64;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 AAAGTGTGATGCTGAGAAC 129
Db 389 AAAGTGTGATGCTGAGAAC 372

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/db_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clones="T485XN"

BASE COUNT 190 a 193 c 136 g 179 t 4 others

ORIGIN

Query Match 9.9%, Score 18; DB 17; Length 702;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 GACACACACGCTGACCA 95

Db 668 GACACACACGCTGACCA 685

RESULT 36

BH556024/c

LOCUS

DEFINITION

sequence. 704 bp DNA linear GSS 14-DEC-2001

ACCESSION

BH556024

VERSION

BH556024.1

KEYWORDS

GSS.

SOURCE

Brassica oleracea.

ORGANISM

Brassica oleracea

REFERENCE

1 (bases 1 to 704)

AUTHORS

Town,C.D., Van Aken,S.,

Utterback,T. and Fraser,C.M.

TITLE

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

Unpublished (2001)

COMMENT

Other GSSs: BGGW27TR

Contact: Chris Town

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@igrr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: single ends

Location/Qualifiers

1..704

/organism="Brassica oleracea"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BGGW27"

/accession="BGGW27"

/notes="ProS1, Site 1, BarXI, 2-3 kb sheared genomic DNA inserted into pGDS1 using BstXI linkers"

BASE COUNT 131 a 180 c 139 g 254 t

ORIGIN

Query Match

9.9%, Score 18; DB 17; Length 704;

Best Local Similarity

100.0%; Pred. No. 64;

Matches 18; Conservative

0; Mismatches 0; Indels

0; Gaps 0;

Qy 112

AAAGTGTGATGCTGAGAAC

129

Db 389

AAAGTGTGATGCTGAGAAC

372

RESULT 37

AQ362915

LOCUS

DEFINITION

nxbs0051A06f, CUGI Rice BAC Library Oryza sativa genomic clone

ACCESSION

nxbs0051A06f

VERSION

nxbs0051A06f.1

KEYWORDS

GSS.

SOURCE

Oryza sativa.

ORGANISM

Oryza sativa

REFERENCE

1 (bases 1 to 708)

AUTHORS

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

TITLE

Homo sapiens genomic DNA, chromosome 21q

JOURNAL

Published Only in Database (1998)

REFERENCE

2 (bases 1 to 702)

AUTHORS

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

TITLE

Homo sapiens genomic DNA, chromosome 21q

JOURNAL

Published Only in Database (1998)

COMMENT

On Feb 5, 1999 this sequence version replaced gi:2754672.

AG003770: Submitted (07-Jan-1998).

FEATURES

Location/Qualifiers

1..702

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clones="T485XN"

BASE COUNT 193 a 203 c 127 g 171 t 6 others

ORIGIN

Query Match

9.9%, Score 18; DB 17; Length 700;

Best Local Similarity

100.0%; Pred. No. 63;

Matches 18; Conservative

0; Mismatches 0; Indels

0; Gaps 0;

Qy 78

GACACACACGCTGACCA

95

Db 572

GACACACACGCTGACCA

589

AUTHORS	Zhang X. Y., Feng J., Li G., Qian H. N., Li X. P., Wu D. C. and Hu Y. C.
TITLE	Differentially expressed transcripts in ovarian cancer identified by mRNA differential display
JOURNAL	Unpublished (1999)
COMMENT	Contact: Zhang XY Gynecologic Oncology Center People's Hospital, Beijing Medical University 133 Fudanmen, Beijing, 100034, China.
FEATURES	<p>source</p> <p>1. 714 Location/Qualifiers /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Homo sapiens ovary epithelium" /clone="N3A018" /cited_type="Ovary epithelium" /cited_by="This SAGE library is from Brain Duke glioblastoma multiforme primary tumor derived from a 51 yo male. Velculescu, V. E., Zhang, L., Vogelstein, B., and Kinzler, K. W. (1995) Serial Analysis of Gene Expression. Science 270, 484-487"</p> <p>BASE COUNT 220 a 144 c 130 g 220 t</p> <p>ORIGIN</p>
Query Match	9.98; Score 18; DB 9; Length 714;
Best Local Similarity	100.0%; Pred. No. 64;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	13 TTCACACAGCGCTGGAA 30
DB	84 TTCACACAGCGCTGGAA 101
RESULT 39	
BIJ172818	
LOCUS	BIJ172818 full length cDNA library, chironomata and young gametophores Physcomitrella patens subsp. patens cDNA clone
DEFINITION	panj3k13 3', mRNA sequence.
ACCESSION	BIJ172818.1
VERSION	GI:18340787
KEYWORDS	EST.
SOURCE	Physcomitrella patens subsp. patens.
ORGANISM	Physcomitrella patens subsp. patens
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Equisetids; Funariidae; Funariaceae; Physcomitrella.
AUTHORS	1. Ibañez J, Ibañez J, Seki M., Kamiya A., Uchiyama I., Nishiyama, T., Fujita, T., Shimizu, Y., Hayashiaki, Y., Shinohara, K., Kohara, T. and Hasebe M.
TITLE	Comparison of the moss physcomitrella patens genome with flowering plants genome
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadaou Shin-I Center For Genetic Resource Information National Institute of Advanced Industrial Science and Technology 1-1-1 Yatai, Mishima Osaka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nia.ac.jp A backbone of the vector is basically from pBlueScript (KS), that was in vivo excised from a modified IFS phage vector (Mo bi Rec. 1) remaining to the end of the backbone. The resulting polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.
FEATURES	<p>source</p> <p>Location/Qualifiers /organism="Physcomitrella patens subsp. patens" /db_xref="taxon:145481"</p>


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VERSION      BHS71181.1  GI:17623020
KEYWORDS
SOURCE       Brassica oleracea
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica
REFERENCE    (base 1 to 63) S., Utterback T. and Fraser C.M.
              Whole genome shotgun sequencing of Brassica oleracea
AUTHORS      Unpublished (2001)
TITLE        Other GSSs: BOHKK72TR
JOURNAL
COMMENT      Contact: Chris Town

BASE COUNT   282 a 139 c 131 g 211 t
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 763;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES      source
              1..763
              /organism="Brassica oleracea"
              /strain="BOHKK72"
              /db_xref="taxon:3712"
              /clone="BOHKK72"
              /clone_lib="BOHKK"
              /notes="Vector: pBIOs1; Site 1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pBIOs1 using BstXI linkers"

BASE COUNT   282 a 139 c 131 g 211 t
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 763;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 TGATGGAGTGTCTCTT 178
Db 728 TGATGGAGTGTCTCTT 745

RESULT 43
LOCUS      B1656335 770 bp mRNA linear EST 12-SEP-2001
DEFINITION 603282642F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5326811 5',
mRNA sequence.
ACCESSION  B1656335
VERSION    B1656335
KEYWORDS   EST 12-SEP-2001
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (base 1 to 770)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
              Email: cga@b6@mail.nih.gov
              Tissue Procurement: Lothar Hemmighausen Ph.D., Priscilla Furth
              Ph.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing: The I.M.A.G.E. Consortium (LLNL)
              Found through the I.M.A.G.E. Consortium information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM1829 row: d column: 12
              High quality sequence stop: 703.

FEATURES      source
              1..770
              /organism="Mus musculus"

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/strain="NWRI"
/clone="IMAGE:5326811"
/clone_lib="NCI CGAP Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
note="Organ: mammary. Vector: pCMV-Sport6; Site 1: Sall;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library: 1000000. Sequenced by: Lothar Hemmighausen/Priscilla Furth.
Providing samples: Lothar Hemmighausen/Priscilla Furth.
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

BASE COUNT   177 a 205 c 281 g 107 t
ORIGIN
Query Match      9.9%; Score 18; DB 13; Length 770;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 CAACAGCTGACGAAGG 100
Db 640 CAACAGCTGACGAAGG 657

RESULT 44
LOCUS      BH738785/C 794 bp DNA linear GSS 20-FEB-2002
DEFINITION BOMPT62TR BO_2_3_XB Brassica oleracea genomic clone BOMPT62, DNA
sequence.
ACCESSION  BH738785
VERSION    BH738785
SOURCE     GSS
ORGANISM   Brassica oleracea
REFERENCE  1 (bases 1 to 794)
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
              Town.C.D., Van Aken.S., Utterback,T. and Fraser.C.M.
              Whole genome shotgun sequencing of Brassica oleracea
              Unpublished (2001)
JOURNAL    Other GSSs: BOMPT62TF
COMMENT    Contact: Chris Town

BASE COUNT   272 a 134 c 110 g 278 t
ORIGIN
Query Match      9.9%; Score 18; DB 17; Length 794;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 AAGGATTTTATTACTTA 59
Db 546 AAGGATTTTATTACTTA 529

FEATURES      source
              1..794
              /organism="Brassica oleracea"
              /strain="Tol0000H3"
              /db_xref="taxon:3712"
              /clone_lib="BO_2_3_XB"
              /clone_lib="BO_2_3_KB"
              /notes="Vector: pBIOs1; Site 1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pBIOs1 using BstXI linkers"

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RESULT 45
CNS032RF
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
071E07 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL267972.1 GI:7989802
VERSION
GSS: genome survey sequence.
KEYWORDS
Tetraodon nigroviridis.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthopterygia; Acanthopterygii; Perciformes; Tetraodontiformes,
Tetraodontidae; Tetraodon.
1 (bases 1 to 1012)
Rost-Crollius,H., Gallon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
1 (bases 1 to 1012)
Rost-Crollius,H., Gallon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
1 (bases 1 to 1012)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
1 (bases 1 to 1012)
Genoscope/Qualifiers
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="071E07"
/clone_lib="G"
note="Genoscope sequence ID : C08G071AC04SP1-end :
PUC-Ori"
BASE COUNT 280 a 181 c 202 g 346 t 3 others
ORIGIN
Query Match 9.9%; Score 18; DB 17; Length 1012;
Best Local Similarity 100.0%; Pred.No.67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 78 GACACACACAGCTGACCA 95
Db 312 GACACACACAGCTGACCA 329

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Search completed: June 9, 2003, 12:46:04
Job time : 1117 secs